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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AX440456
Xu,J., Mitcham,J.L., Harlocker,S.L., Dillon,D.C., Secrist,H., Lodes,M.J., Algate,P.A., Fling,S.P., Mannion,J., Benson,D.R. and Carter,D.	Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1	Homo sapiens	human.		AX440456.1 GI:21665266	AX440456	4.	AX440456 814 bp DNA linear PAT 28-JUN-2002	

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type II membrane protein.
Homo sapiens gastric adenocarcinoma
clone_lib:pKA1-meta-1 clone:HP10390.
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Selection of cDWAs encoding putative type II membrane pr
the cell surface from a human full-length cDNA bank
Gene 228 (1-2), 161-167 (1999)
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Sequence 17:
AX464040
AX464040.1
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Eukaryota; Me
Mammalia; Eut
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                                                                                                                                                                                                                                                    Genentech
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                                                                                                                                                                                                                                                              Patent:
                                                                                                                                                                      Similarity
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                           WO 0140466-A 173 07-JUN-2001;
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                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
316 c 379 g 25
                                                                                                                                                                                                                                          Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae;
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Bornhauser, B.C., Olsson, P.-A. ai NSAP is a novel saposin-like prostimulates neurite outgrowth
                                                                                                                                                                                                                                          Direct Submission
Submitted (13-APR-2001) Neuroscience,
Husargatan 3, Uppsala 75123, Sweden
Location/Qualifiers
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Olsson, P.-A. and Lin
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Homo sapiens
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                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/map="12915"
419. .967
/note="NSAP; encodes a type 2 membrane signal and a putative ER retention motif"
/codon_start=1
/product="saposin-like protein"
/protein_id="AAK38148.1"
/db_xref="GI:20196199"
/translation="MKGMUMALLIGALLGTAWARRSQDLHCGACRALVDELEWEIAQ
VDPKKTIQMGSFRINPDGSQSVVEVPYARSEAHLTELLEEICDRMKEEGEQIDPSTHR
KNYVRVVGRNGESSELDLQGIRIDSDISGTLKFACESIVEEVEDELIEFFSREADNVK
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saposin-like protein
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Eukaryota;
Mammalia; E
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IMAGE: 2650612,
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Eutheria;
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Chordata;
Rodentia;
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CAAAGTGAAAGTCCAGCGGTCTGCCAGCGCTTGGGCCACGGCGGCGGCCGCCCTGGGACCAAA 77
Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.llr Series: IRAK Plate: 5 Row: b Column: 23
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 5 Location/Qualifiers
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Direct Submission
Submitted (22-MAY-2001) National Institutes of Health, Mammalian Submitted (22-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Institutes, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Baylor College of Medicine Human
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar H
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Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
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VDPKKTIOMGSGSVEVPYARSBAHLTELLEEVCDRMKEYGEQIDPSTHR
KNYVRVVSRNGESSELDLQGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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RS MuznyD. M., Adams (C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooke, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S. B., Erowa, M., Brown, E., Brown, M., Bryant, N.P., Bunch, C., Carter, M., Cavazos, S.R., Chacko, J., Chavaz, D., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferrayuto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunarathe, P., Hale, S., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hubyk, S., Hume, J., Jackson, L., Kureshi, A., Landry, N., Jolivet, S., Joudah, S., Karlsson, B., Kally, S., Khan, U., King, L., Korvah, J., Louiseged, H., Lozado, R.J., Lux, J., Lucler, A., Lucler, R., Luna, R., Mastinez, E., Massey, E., Mawhiney, E., McLeed, M.P., Meador, M., Manch, P., Masdor, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Mershwari, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
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Center clone name: RP11-764L14

Center clone name: RP11-764L14

Sequencing vector: M13; L0881

Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 161278 bases at least 030

Consensus quality: 170806 bases at least 030

Consensus quality: 174843 bases at least 020

Estimated insert size: 168803; sum-of-contigs estimation

Duality coverage: 6x in 020 bases; syarose-fp estimation

Quality coverage: 5.8x in 020 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

*NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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Score 590.4; DB 2; Pred. No. 3.2e-141;
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Length 158198;

Lehner, J.

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RESULT 7
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Mus musculus putative Unpublished 2 (bases 1 to 1017)
                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 1017)
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                             O'Hara, P.
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                  ACCATGCCCTGCACATATCGCATGATGAGCTATGAACCACTGGAGCAGCCCAC----
                                                                                                                                                     CCCGCTCAGAGGCCCACCTCACAGAGTTGCTTGAGGAGGTGTGTGACCGAATGAAGGAGT
                                                                                                               ATGGAGAATCCAGTGAACTAGACTTACAGGGCATCCGAATTGACTCAGATATCAGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (14-SEP-1999) Biomolecular In
Inc., 1201 Eastlake Ave. East, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheppard, P., Jelinek, L., O'Hara, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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250 c 315 g 204 t
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/product="putative secreted
/protein_id="AAF01433.1"
/db_xref="GI:6014636"
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/db_xref="dbEST:AA049839"
/db_xref="taxon:10090"
/clone="IMAGE:476061"
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le, WA 98102,
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CCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCCAGGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-SEP-1999) Biomolecular Informatics, ZymoGenetics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'Hara, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 649)
Sheppard, P., Jelinek, L., Whitmore, T., Blumberg, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheppard, P., Jelinek, L., Whitmore, T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 649)
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                                                                                                                                                                                                                                                                                                                                                                                                          /gene=
                                                                                                                                                                                                                                                                                            /translation="mkGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQ
VDPKKTIQMGSFRINPDGSQSVVEVTVTVPPNKVAHSGFG"
150 c 171 g 149 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="dbEST:R15306"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                    /product="putative secreted protein ZSIG9"
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/db_xref="GI:6014632"
                                                                                                                                                                                                                                                                                                                                                                                             /gene-"ZSIG9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .649
                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone-"IMAGE: 29675"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
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98.1%;
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Pred. No. 6.4e-69;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: p Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6014631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby.K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nc1.n1h.gov
Contact: MGC help desk
Email: cgapbs-remail.n1h.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 824)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: National Institutes of Health
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BC001027.1
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IMAGE:3344788,
                     221
                     ø
               /product="transmembrane protein 4"
/protein_id="AAH01027.1"
/protein_id="AAH01027.1"
/db_xref="GI:1265403"
/translation="MMGWGWLALLIGALLGTAWARRSQDLHCGACRALVDELEWEIAQ
/translation="MMGWGWLALLIGALLGTAWARRSQFG"
VDPKKTIQMGSFRINPDGSQSVVEVTVTVPPNKVAHSGFG"
194 c 233 g 176 t
                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="MGC.151"
                                                                                                                                                                                      /note="Vector:
                                                                                                                                                                                                         /tissue_type="Eye, reti
/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="LocusID:10330"
                                                                                                                                                                                                                                                                       /clone-"MGC:1545 IMAGE:3344788"
                                                                                                                                              codon_start=1
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clone MGC:1545
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AX440375
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                    GCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCCAGGTGGACCCCCAAGAAG
                                                                                                                                                                                                                                                               CTGGGGCCAAAGTGAAAGTCCAGCGGTCTGCCCAGCGCTTGGGCCACGGCGGCGGCCCTGG 70
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 228 from Paten:
AX440375
AX440375.1 GI:21665185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: WO 0190154-A 228 29-NOV-2001; CORIXA CORPORATION (US)
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Lodes,M.J., Algate,P.A., Fling,S.P.,
                                                                                                                                                                                                                                                                                                                          Similarity
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142 c 152 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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95.8%;
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Pred. No. 1.2e
1; Mismatches
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Pred. No. 1.1e
1; Mismatches
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                                                                                                                                                                                       Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davis, C., Ding, Y., Ding, Y., Dinh, H.H., Douthwalte, K.J., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., Earnhart, C., Edgar, D., Flagg, N., Forcha, S., Durbin, K.J., Earnhart, C., Edgar, D., Flagg, N., Forcha, S., Durbin, K.J., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Forcha, S., Durbin, K.J., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Forcha, S., Hamilton, K., Garriell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Garriell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Kovah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, R., Maylar, P., Martin, R., Martindale, A., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Marhiney, E., McLeod, M.P., Meador, M., Morgan, N., Woygen, N., Nguyen, A., Nguyen, N., Nguyen, A., Nguyen,
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              Worley, K.C.
Direct Submission
Submitted (11-MAR-2000) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                              Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                     Unpublished
                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 12 clone RP11-348M3, WORKING SEQUENCE, 12 unordered pieces.
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1 (bases 1 to 155023)
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TITLE
                                        Matches
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Best Local Similarity
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306 AGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACC 365
                                      206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 3, 2002 this sequence version replaced g1:20335511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-primer Bodipy: 5% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 141522 bases at least 030
Consensus quality: 147097 bases at least 030
Consensus quality: 150442 bases at least 020
Estimated insert size: 15070 b; sum-of-contigs estimation
Consensus quality: 15040 by Sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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1. .155023
                                                                                                                                                          /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/chromosome-"12"
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36207 c 35987 g 41693 t
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42263: contig of 10385
42363: gap of unknown 1
51104: contig of 8741 b
51204: gap of unknown 1
68306: contig of 17102
68406: gap of unknown 1
109481: contig of 41075
109581: gap of unknown 1
155023: contig of 45442
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                                                                                                                                                                                 Bouck J. Bowle, S. Brieva, M., Brown, E., Brown, M., Brynt, N.P., Boulay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carren, M., Carter, M., Cavasos, S.R., Chacko, J. Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, C., Davy-Carroll, L., Dederich, D.A., David, R., David, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., David, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delyado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Filag, N., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Hagris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudsh, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvsh, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvsh, J., Kovar, C., Karlsson, E., Miner, G., Miner, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Mosser, M., Roysh, R., Pirlmus, E., Pull, L., Quiles, M., Ren, Y., Peters, J., Pickens, R., Pirlmus, E., Pull, L., Quiles, M., Ren, Y., Rives, M., Roysh, R., Roysh, R., Roysh, R., K., Tang, H., Stanley, H., Stanley, H., Stanley, H., Stone, H., Sutton, A., Statley, H., Stone, H., Sutton, A., Walle, S., Warten, R., Washington, C., Watlington, S., Wullen, S., Wallen, D., Wallen, 
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SEQUENCE, 5 unordered con
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                                                                                                      Direct Submission
                                                                                                                                   Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Pr
1 (bases 1 to 182350)
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_BRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Best Local Similarity
Matches 206; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-JUL-2000) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
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3 (bases 1 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: Plasmid;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 15% of reads
Chemistry: Dye-terminator Big Dye: 85% of reads
Chemistry: Dye-terminator Big Dye: 85% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 179279 bases at least Q40
Consensus quality: 180581 bases at least Q20
Consensus quality: 181073 bases at least Q20
Estimated insert size: 174258; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: HBWI
Center clone name: RP11-977G19
Center clone years Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                       /chromosome="12"
/clone="RP11-977G19"
45416 c 43855 g 46174 t
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/db_xref="taxon:9606"
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2993: gap of unknown length
6686: contig of 3693 bp in length
6786: gap of unknown length
17251: contig of 10465 bp in length
17351: gap of unknown length
17351: gap of unknown length
85894: contig of 68543 bp in length
85994: gap of unknown length
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Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buray, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H.,
Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
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Davila, M.L., Davis, C., Coyle, M.D., Dederich, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Golthwaite, K.J., Desper, H., Dugan-Rocha, S., Durbin, K.J.,
Gorrell, J.H., Gercia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Garcia, A., Garner, T., Garza, N., Gill, R.,
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Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kractovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Kureshi, A., Landry, N., Leal, B., Louse, R., Martinez, E.,
Massey, E., McLeod, M., Laud, R., Martinez, E.,
Massey, E., McLeod, M., Martinez, E.,
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                                                                                                                                                                                           Submitted (15-FEB-2000) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sutton A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Teifrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wieczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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Homo sapiens chromosome 12 clone RP11-183H16, WORKING DRAFT
                                                                               Worley, K.C.
Direct Submission
                                                                                                                                                               Baylor Plaza, Houston, 3 (bases 1 to 184762)
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Barbaria,J., Benton,J., Bimage,K., Blankenburg,K.,
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(24-AUG-2002) Human Genome Sequencing Center, Department
lar and Human Genetics, Baylor College of Medicine, One
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                                                                                                                               Baylor Plaza, Houston, 18 //טיטי, טייה on Aug 4, 2002 this sequence version replaced gi:22094227.
Genome Center
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NOTE: This is a "working draft" sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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ATATTAGCGGCACCCTCAAGTTTGCG
                                                                                                                                                                     188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-JAN-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
On Jan 26, 2002 this sequence version replaced gi:18201765.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
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Harbor, NY 11724, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for Mus musculus, clone RP23-104010, complete
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Mammalia; Eutheria; Rodentia;
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48671 c 49663 g 56477 t
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48132...48165
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/db_xref="taxon:10090"
/clone="RP23-104010"
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                                                                                                                                                                                    RES MIZENJO, D.M., Addams, C., Addio-Oduola, B., All-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox.C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, S., Hart, M., Halloway, C., Hollins, B., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hernandez, J., Hong, E., Howards, C., Hart, M., Halloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hame, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kally, E., Khan, U., King, L., Kortah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Levis, L.C., Levis, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R., J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Massey, E., Mawhiney, S., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Massey, E., Mawhiney, S., Parke, A., Payton, B., Peery, J., Perez, L., Peters, L., Peters, L., Levis, L., Lichter, A., Lucier, R., Mayser, M., Thomas, N., Thomas, S., Wareron, R., Wang, O., Wattington, S., Walles, M., Thomas, S., Wallington, S., Wallington, S., Wallingto
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Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 101666)
                                                                                        Worley, K.C.
Direct Submission
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                                                                                                                                                  Unpublished
                                                                                                                                                                         Direct Submission
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center project name: GQXY
Center clone name: CH230-319E6

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 60229 bases at least Q40
Consensus quality: 63959 bases at least Q30
Consensus quality: 66730 bases at least Q20
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Best Local Similarity 90.3%;
Matches 186; Conservative
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1. organism="Rattus norvegicus"
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/clone="CH230-319E6"
/a 22934 c 23569 g 23059 t 7.
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80133 contig of 3296 bp
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86731 contig of 3509 bp
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93107 contig of 3078 bp
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Search completed: March Job time: 2658.55 secs

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     2185239 segs, 1125999159 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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702.4	749.4	749.4	750.4	750.4	750.4	750.4	804.6	805.6	Score
87.1	93.0	93.0	93.1	93.1	93.1	93.1	99.8	100.0	Query Match
714	1210	1180	814	814	814	814	806	806	Query Match Length DB
20	22	20	24	24	24	21	20	21	DB
AAX97884	AAS21330	AAX22112	ABK09772	ABL41995	ABK52765	AAZ38327	AAX06969	AAZ08293	ID
Human secreted pro	Human cDNA sequenc	Human secreted pro	Human ovarian tumo	Nucleotide sequenc	cDNA encoding tran	Human transmembran	Human secretory pe	Human Zsig9 gene e	Description

Human prostate exp			483	6.3	50.4	45	
			311	6.4	51.4	44	
Drosophila melanog			81	٠	53.4	4	
Mouse spliced tran				6.7	53.8	42	
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			2724	15.0	121	40	
			272	•	121	39	
			253	•	121	38	
			253		121	37	
cancer rela			12	•	126		O
Gene #1334 used to	4 ABN94836	6 24	126	15.6	126	35	0
Human polynucleoti			49	•	130.8	34	
cancer rela			14		147	ω	
#1335 used	4 ABN94837		14		147	32	
secreted			26	•	151.8	31	
secreted	1 AAC24962		21	•	163.8	30	
			35	•	173.8	29	
Human ovarian tumo			56		237.8	28	
CO.			41	•	267	27	
) AAX06971		41	•	267.6	26	
breast			116	٠	271.4	25	
			48	•	272.4	24	
			64	•		23	
WO9901020 Seq ID 3			108	•	284.2	22	
Human secreted pro) AAX97836		79	٠	286	21	
O .			71	•	288	20	
			64	•	306.8	19	
secreto			64	•	308.6	18	
			59	•	318.6	17	
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ortholog c			106	74.	599	13	
secretory			106		599	12	
CO.	ABK360		65	80.	646.4	11	
Human secreted pro) AAX97837		83		688.4	10	

ALIGNMENTS

RESULT 1 AAZ08293

AAZ08293 standard; DNA; 806 BP.

AAZ08293;

07-FEB-2000 (first entry)

Human Zsig9 gene encoding secretory protein variant-4.

Secretory protein-9; Human Zsig9; chromosome 12q15 region; variant; overexpression; antagonist; antibody; antisense nucleotide; tumour; treatment; receptor; radio-label; fusion; polypeptide toxin; technique; down-regulation; probe; dlagnostic; therapeutic; cancer; brain; liver; detection; stomach; lymphoma; alternative splicing; allelic variation; silent mutation; дg

Homo sapiens.

Synthetic.

TO NOT THE FEBRUARY SOUND THE FE mat_peptide sig_peptide CDS /note- "0 104..163 /*tag= 1 164..649 Location/Qualifiers /*tag= c /label= Mature_Zsig9_protein_variant-4 /product= "Zsig9 secretory protein variant-4"
/note= "Overexpressed in tumours" *tag= ٥

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Matches 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-9, Zsig9 that arises due to alternative splicing, allelic variation or silent mutations that result in amino acid changes. This sequence is mapped to the human chromosome 12q15 region. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to Zsig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to Zsig9 and it may be radiolabelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of Zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding Zsig9. The Zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma, etc., at an early stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 806 BP; 229 A; 183 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 33-35; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting tumors using antibodies, antagonists and nucleotides to secretory protein-9 (Zsig9) -
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                                                                                TGACCGGATGAAGGAGTATGGGGAACAGATTGATCCTTCCACCCATCGCAAGAACTACGT
CTCAGATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGGAATACGAGGA
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                                               ACGTGTAGTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGA
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03-JUL-1997;
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19-MAY-1998;
17-JUN-1998;
                                  New mammalian secretory peptide-9 (2sig9) enhancer for placenta, liver and heart, a
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                                                                             SR,
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                                                                                                                                                                                                                                                                          growth enhancer;
                                                                             Jelinek
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            73-74; 85pp;
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97US-0051704.
97US-0888088.
98US-0081338.
98US-0085983.
98US-0089899.
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This

CDNA

clone

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human

secretory

peptide-9,

မ္ပ zsig9,

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variant (see AAW88474). zsig9 (see also AAW88469) is overexpressed in thuman brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors. Thus, Zsig can be used as an indicator for cancer. Zsig9 cDNA was discovered in a placenta clone from a full-term pregnancy cDNA library which contained an expressed sequence tag (see AAX06971). The invention provides colone tag sequence tag (see AAX06971). The invention provides colone trom it can be used as an indicator of the zsig9 polypeptides (see AAX069671) and the processed forms, the zsig9 gene, or probes derived from it, can be used to determine if Zsig9 gene, or probes derived from it, can be used to determine the zsig9 gene, or probes derived zsig9 can be used as diagnostic agents to determine the presence of zsig9 can be used as diagnostic agents to determine the presence of zsig9, and thus the presence of cancer. They can also be labelled with radioisotopes or fused with toxins and used to treat tumours which overexpress zsig9. Antisense nucleotides derived from zsig9 cDNA can also be used to enhance the growth or development of the proteins can be used to enhance the growth or development of the
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                                                                                           GCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATGATGAGCTATGAACCACTGG
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No. 2.1e-193;
smatches 1; Indels 0;
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                    Query Match
Best Local S
Matches 754
                                                                                                                                                                                                                                                                                                                                              This sequence represents the human cDNA clone HP10390 which encodes a 20 kD protein with one putative transmembrane domain in the N-terminus. The cDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists
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(PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins with transmembrane domains, involved in control of cell prollferation and differentiation, useful for treating e.g. cancer or inflammation -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 106-107; 114pp; English.
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                                                                                                                                                                                                               A; 194 C; 241 G; 169
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Score 750.4; I Pred. No. 1.1e 1; Mismatches
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The invention relates to modulators of a cancer-related genes. Also classribed are: (1) processes for identifying an anti-neoplastic agents comprising contacting a cell exhibiting neoplastic activity with a compound first identified as a cancer related gene modulator, and detecting a decrease in the neoplastic activity. (2) a process for determining the cancerous state of a cell by determining an increase in the level of expression of at least one gene, where an elevated expression relative to a known non-cancerous cell indicates a cancerous state or potentially cancerous state. The anti-neoplastic agent is state or potentially cancerous state. The anti-neoplastic agent is useful for treating cancer or for protecting an animal against cancer. The immunogenic composition is also useful for treating cancer in an animal, where the composition elicits the production of cytotoxic Tlymphocytes specific for the immunogenic composition. Preferably, the animal is a human. The cancer-linked genes and polypeptides are also useful as targets for cancer therapy or chemotherapy. The present sequence represents a cancer-linked gene located on chromosome 12, which encodes transmembrane protein 4.
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P-PSDB;
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                                 Antibody preparation by inoculation of an animal with a vector expressing a fusion protein of an antigen on the C-terminal si transmembrane domain for use as drugs, diagnostic reagents and
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                                                                                                                                                                                                                                                                                                                                                                                GACCAAAGGTGGAGCAACCCCGTTACCCTAAARATGAAAGGCTGGGGTTGGCTGGCCCTG
                                                                                                                                   AGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATT
                                                                                                                                                                      GGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATATT
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GTTTTTACTGAAATTAACTGAAAAATATGAAACCAAAAGTA
          GTTTTTACTGAAATTAACTGAAAAAATATGAAACCAAAAGTA 772
                                GAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAGAT
                                                                                                                                                                                                        Similarity
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Pred. No. 1.1e
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RESULT 6 ABK09772

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Best Local S
Matches 754
                                                                                                                                                                                                                       and for treating ovarian cancer in a patient. An antigen presenting cell that expresses the sequences is useful for treating ovarian cancer by incubating CD4+ and/or CD8+ T cells isolated from a patient. The T cells can then be proliferated and administered to the patient to inhibit the development of cancer. The DNA sequences are useful as probes or primers for nucleic acid hybridisation, to direct expression of a polypeptide in appropriate host cells. Detecting the presence of a cancer in a patient involves obtaining a biological sample from the patient, contacting the biological sample with an agent that binds to the protein, detecting the amount of protein that binds to the agent, comparing the presence of cancer. Sequences ABK09464-ABK09802 represent PCR primers and CDNA molecules encoding ovarian tumour proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-2000;
21-JUN-2000;
03-AUG-2000;
01-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide encoding a polypeptide comprising a portion of an ovarian tumour protein. The sequences of the invention are useful for stimulating an immune response and for treating ovarian cancer in a particular and immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 253-254;
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian tumour protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-097641/13.
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                                                                      GACCAAAGGTGGAGCAACCCCCGTTACCCCTAAARATGAAAGGCTGGGGGTTGGCTGGCCCTG 130
                        CTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGA
                                                therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ovarian cancer
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PA, Fling
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herapy; CD4+ T cell; CD8+ T cell; PCR primer.
                                                                                                                                                                Similarity
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; 2000US-211457P.
; 2000US-213673P.
; 2000US-223288P.
; 2001US-272790P.
                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mannion
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                                                                                                                                                  Score 750.4; DB 24; Pred. No. 1.1e-179; 1; Mismatches 7;
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Benson
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12-SEP-1997; 01-JUL-1997; 01-JUL-1997; 12-SEP-1997;

97US-0058663. 97US-0051381. 97US-0051480. 97US-0058598.

30-JUN-1998; 14-JAN-1999

98WO-US13608

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                                                                                                                                                  Human; secreted protein; gene therapy; protein therapy; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; schizophrenia; immunological disorder; mood disorde immune deficiency disease; respiratory disorder; arthritis; skeletal; haematopoietic disorder; neural; osteoporosis; metabolic disorders; cardiovascular; endocrine; gastrointestinal; asthma; diagnosis; ds.
                                                                                                                                                                                                                                                           18-MAY-1999
                                                                                                              WO9901020-A2
                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders, schlzophrenia, immunological disorders, immune deficiency diseases. (AIDS), mood disorders, respiratory disorders, arthritis, asthma, chaematopoletic disorders, respiratory disorders, arthritis, asthma, chaematopoletic disorders, cardiovascular disorders, endocrine disorders or gastrointestinal disorders. The polypeptides are also useful for identifying their binding partners. The present sequence represents a gene encoding a human secreted protein (see descriptor line for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acid sequences (AAX22111 to AAX22134) encoding human secreted proteins (AAV01135 to AAV01136). The secreted protein gene sequences are deposited with the ATCC under deposit number ATCC 209118. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, immune deficiency diseases or blood
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DB; AAY01136, A#
                                                                                                                                                                                                                                              GCATGCAGGGCTCTGGTGGATGAACTAGAATGGGGAAATTGCCCCAGGTGGACCCCCAAGAAG
                              CCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATG
                                                                                                                                                                              CTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGA
GGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATATT
                                                                                                                                                                                                                             GCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCCAGGTGGACCCCCAAGAAG
                                                                                                                                                                4; Page 117; 179pp; English
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Pred. No. 2.2e-179;
1; Mismatches 7;
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RESULT 8

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PFR 01-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breast; prostate; cervical; tumour necrosis factor-a cartilage; ear; proliferation; glucose; free fatty a adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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t; prostate; cervical; tumour
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CC PRO polypeptides, to link bioactive molecules to detect other companies of the propertides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC Some of the 275 sequences are also useful to stimulate the release of CC proliferation or differentiation of chondrocytes, the proliferation or correct cells, the release of proliferation or differentiation of chondrocytes, the proliferation of cromparing procession in pericyte cells, the release of proteoglycans from CC of Tlymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells corrected (PBMCs) or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC to factor VIIA. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The polynocleotides encoding CC PRO polypeptides can be used to assays to identify CC molecules can be used to generate probes, antisense RNA,DNA, CC transgenic or knock cut animals and can be used to generate RNA,DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 753
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transgenic or knock c
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                                                                                                                             CCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATG
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GGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATATT
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                                        Conservative
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Tumas
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A, Godowski PJ, Gurney AL,
Tumas D, Watanabe CK, Wood
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1; Mismatches
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y AL, Sherwood S;
Wood WI, Zhang Z
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13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
                                              AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAY36129-Y3622) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used diagnostic, forensic, gene therapy and chromosome mapping procedures Uses also include design of expression vectors and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                       Bougueleret L,
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                                                                                                                                                                                                                                                                                  cDNAs encoding secreted
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97US-0066677.
97US-0069957.
98US-0074121.
98US-0081563.
98US-0096116.
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Best Loc
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                27-MAY-1999
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Local Similarity yo...
706; Conservative
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 98WO-IB01862
                                                          therapy;
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17-DEC-1997;
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13-APR-1998;
10-AUG-1998;
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P-PSDB; AAY36153.
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                                  CTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGA
                                                                                                                                                                                                                                              GACCAAAGGTGGAGCAACCCCGTTACCCTAAARATGAAAGGCTGGGGTTGGCTGGCCCTG
                                                                GGGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATAT
                                                                                                                          GCCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGAT
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              TTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAG
                                                                                             GCATGCAGGGCTCTGGTGGATGAAACTAGAATGGGAAATTGCCCCAGGTGGACCCCCAAGAA
       TTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAG
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                                                                                                                                                                                                                                                                                                           Conservative
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97US-0069957.
98US-0074121.
98US-0081563.
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97.6%;
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; Pred. No. 4.9e
1; Mismatches
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RESULT 11
ABK36007
The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple scherosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. hemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK36232 represent the cDNA sequences of the invention that encode for novel human contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacobs K,
Merberg D,
Clark HF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Six hundred and twenty three polynucleotides derived from a variety human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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Treacy M,
Fechtel K,
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Agostino MJ, Bowman MR, Spaulding V, Wong
Howes SH, Resnick RJ, Gulukota K, Graham :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel human secreted protein
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Best Local Similarity
Matches 650; Conserv
                  mat_peptide
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                                                                                                          Secretory peptide cancer; therapy;
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                                                                                                                                         Mouse secretory peptide-9 (Zsig9) orthologue cDNA
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                                                                                                                                                                                                      standard; cDNA; 1069
                                                                                                          peptide-9; Zsig9;
nerapy; diagnosis;
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                  /*tag= b
418..903
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358..417
                                                          Location/Qualifiers 358..906
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                                                                                                          orthologue; mouse; tumour marker; growth enhancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 1.8e-153;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                        This cDNA clone encodes novel mouse secretory peptide-9, or 2sig9 (see AAW88476), an orthologue of novel human 2sig9 (see AAW88469). Human 2sig9 is overexpressed in a number of tumours including brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors, and thus can be used as an indicator for cancer. The invention provides polyncleotides (see AAX0698-70) cencoding 2sig9 polypeptides (see AAW88469-77) including mature polypeptides, other processed forms, variants and the mouse orthologues. The 2sig9 gene, or probes derived from it, can be used to determine if Zsig9 is present on chromosome 10, and if a mutation has occurred. Antibodies raised against 2sig9 can be used to determine if Zsig9 is present on chromosome 10, and if a radioisotopes or fused with toxins and used to treat tumours thus the presence of cancer. They can also be labelled with radioisotopes or fused with toxins and used to treat tumours which overexpress 2sig9. Antisense nucleotides derived from 2sig9 proteins can be used to enhance the growth or development of the placenta, heart or liver.
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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03-JUL-1997;
03-JUL-1997;
19-MAY-1998;
19-MAY-1998;
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DB; AAW88476.
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CCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGT
                                     GGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAAGGTGGACCCCAAGAAGAACATTC
                                                                                                                                                                                                         GGTGGAGCAACCCCGTTACCCTAAARATGAAAGGCTGGGGTTGGCTGGCCCTGCTTCTGG
                                                                                        GGTGGAGCGACCCTGTTACACTAAAGATGAAAGGCTGGGGTTGGCTAGCCCTACTTTTGG
                                                                                                                                                                                                                                              CANAGTGAGAGTCCGGCTGCTTTCCAGAGCCTGGGCCACGGCGGCGGCGGCGGCAGCAGA
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                                                                                                                                                                                                                                                                                                 690;
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                                                                                                                                                                                                                                                                                                            Similarity
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nilarity 87.7%;
Conservative
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Pred. No. 2.1e-141;
1; Mismatches 86;
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heart, and
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                                                                                                                                                                                                                                                                                                                      Length 1069;
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RESULT 13
AAZO8294

LID AAZO8
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AC AAZO8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; antisense nucleotide; tumour; treatment; receptor;
radio-label; polypeptide toxin; down-regulation; diagnostic;
therapeutic; probe; cancer; brain; liver; detection; stomach
lymphoma; ds.
                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secretory protein-9;
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  (ZYMO ) ZYMOGENETICS
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418..903
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Mature_Zsig9_protein_variant-4
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Best Local Similarity 87.7
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present DNA sequence is an ortholog encoding the secretory protein-9, zsig9 derived from mouse. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to zsig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to zsig9 and it may be radio-labelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding zsig9. The zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma etc., at an early stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1069
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TGGCTTGATGGATCACCCCCAGGAGGGGAAAATGGTGGCAATGCCTTTTATATATTATGT
                                   ACCATGCCCTGCACATATCGCATGATGAGCTATGAACCACTGGAGCAGCCCAC----AC
                                                                               TTTCCCGAGAGAGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAGATCTTTGTG
                                                                                                                              CCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCT
                                                                                                                                                                          ATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATATTAGCGGCA
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                                                                                                                                                                                                                                                                           CCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGT
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DB; AAY15136.
                                                                    TCTCCAGAGAGGCTGACAACGTTAAAGACAAACTTTGCAGTAAGCGGACAGATCTATGTG
                                                                                                                 CCCTCAAGTTTGCGTGTGAGAGCATTGTGGAAGAATACGAGGATGAGCTTATCGAATTCT
                                                                                                                                                                ATGGAGAATCCAGTGAACTAGACTTACAGGGCATCCGAATTGACTCAGATATCAGCGGCA
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                      tumors using antibodies, es to secretory protein-9
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Pred. No. 2.1e-141;
1; Mismatches 86; Indels 10
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                   This sequence represents the coding sequence of human cDNA clone H910390 which encodes a 20 kD protein with one putative transmembrane domain in the N-terminus. The cDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transforme with these nucleotides may be used to screen for agonists and antagonist which are potentially useful therapeutically.
                                                                                                                                                                           Claim
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P-PSDB; AAY52391.
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                                                                                                                                                                                                            Human proteins with transmembrane domains, proliferation and differentiation, useful
                                                                                                                                                                                                                                                                                                                                                    28-APR-1998;
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                                                                                                                                                                                                                                                                                                              (SAGA ) SAGAMI CHEM RES CENT. (PROT-) PROTEGENE INC.
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                                                                                                                                                                          English.
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Query Match
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Score 546; DB 21; Pred. No. 3.9e-1

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CC AAA43426 to AAA45925 represent specifically claimed secreted expressed CC sequence tags (SESTs), isolated from human, mouse, chicken and rat CC tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; analgesic; haemostatic; intrombolytic; antiinflammatory; CC chemokinetic; analgesic; haemostatic; intrombolytic; antiinflammatory; CC control; vulnerary; antiulcer; osteopathic; neuroprotective; CC antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective; CC anticonvulsant; and antidepressant. The sESTs can be used for gene CC identification and isolation of full-length cDNAs and genomic DNA CC molecules which correspond to the SESTs, proteins encoded by the sESTs are useful as probes for the CC identification and isolation of full-length cDNAs and genomic DNA CC molecules which correspond to the SESTs, proteins encoded by the sESTs are useful as probes for the CC identification and isolation of full-length cDNAs and genomic DNA CC (multiple sclerosis, insulin dependent diabetes), allergic conditions CC (multiple sclerosis, insulin dependent diabetes), allergic conditions CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Crohn's Cdisease), tumours, bacterial, fungal or viral infections, dependent of automoros, bacterial, fungal or viral infections, dependent and correctors, dependent of appression and correctors. Secured to AAA45931 represent invention.
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Merberg D,
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APPLICATION NUMBER: 60/0 APPLICATE: 1997-00-FILING DATE: 1997-08-: APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ APPLICATION FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 6 FILING DATE: 1997-05-FILING DATE: 1997-01 APPLICATION NUMBER: FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: NUMBER: 60/0: 1997-09-05 NUMBER: 60/048,964: 1997-06-06 NUMBER: 60/056,862 : 1997-08-22 NUMBER: 60/056,875: 1997-08-22 1997-08-22 1997-05-23 1997-08-1997-08-1997-08-1997-08-22 NUMBER: 60/056,894 60/056,884 18-22 60/057,650 60/056,908 60/056,887 60/047,614 60/047,594 60/047,590 60/047,586 60/047,585 60/047,588 60/047,599 60/057,761 60/056,892 60/056,845 60/056,631 60/056,864 60 60 60/047,595 60/056,910 /056,636 /056,911 /056,874

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US-08-553-367A-1
                                                            US-08-553-367A-1
    Best Loc
Matches
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Best Local (
                             Query Match
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APPLICANT: Theodo
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                                                                     HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUIDIT
IMMEDIATE SOURCE:
CLONE: Clone pBl1
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: NO. 5939
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GANUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1747 CCAGGGGTGGGAATTTTTTTTTAATATGTGTCATGAATAAAGTTGTTTTTGAAAAKAAAA 1806
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lee Cheng
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                Local
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ER APPLICATION NUMBER: 60/057,669
ER FILLING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/049,610
ER FILLING DATE: 1997-06-13
ER APPLICATION NUMBER: 60/061,060
ER FILING DATE: 1997-10-02
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72; Conser
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Similarity 63.068; Conservative
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                                                                                                                                                                                                               1395 base pairs
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                                                                                                   Cucurbita maxima
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             5.5%;
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Score 44.6; DB 2;
Pred. No. 0.0091;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                   49/FD4.5MZ
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                             Length 1395;
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Gaps
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
NITI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucurbita maxima
IMMEDIATE SOURCE:
CLONE: Clone pB11
US-09-295-306-1
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                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 49/DIV-FD4.5MZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/553,367 FILING DATE: No. 6198021ember 27, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                             692 CAGGAGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTTACTGAAATTAACTGA 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 CAGGAGGGGAAAATGGTGGCAATGCCTTTTATATTATTATGTTTTTACTGAAATTAACTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2033 K S CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                  1395 base pairs
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                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                           5.5%;
63.6%;
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                                                                                                                            0;
                                                                                                                                           Score 44.6; DB 4
Pred. No. 0.0091;
                                                                                                                            Mismatches
                                                                                                                                                      DB 4;
                                                                                                                                                          Length 1395;
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CLONE: Clone pB11
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-734-719-1
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                                                        US-08-232-463-14/c
                                                                          RESULT 5
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US-09-734-719-1
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Best Local S
Matches 68
Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09734719
Patent No. 6455675
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                   1349
                                                                                                                                                                                                         1289 CTGGAAGTTGCAATTAAAATAAACCCCTTTAATATCACATGTTCTTACTTTGCTCAAAAAA 1348
                                                                                                                                                                    692 CAGGAGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTTACTGAAATTAACTGA 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/295,306
FILING DATE: April 21, 1999
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6455675ember 27, 19
APPLICATION NUMBER: PCT/EP94/01664
FILING DATE: May 24, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
PEFFERENCE TO NUMBER: 40,949
                                                                                                                                                                                                                                                                                    Local Similarity
les 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 202-721-8200
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                                                                                                                                 ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/734,719 FILING DATE: 13-Dec-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1395 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-721-8250
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STATE: D.C.
                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                  Score 44.6; DB 4;
Pred. No. 0.0091;
0; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                               Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
1200
                                                                                                                      1260
                                                                                                                                                                                 1320
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                        669
                                                                                                                                                   609
                                                                                                                                                                                                          549 TTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAG 608
                                                                                                                                                                                                                                                                    489 TTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCA 548
                                                                                                                                                                                                                                                                                                                               429 TGGGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                            Local Similarity 1.3%; hes 5; Conservative
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ZIP: 22313-0299
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STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 899149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                         ATCTTTGTGACCATGCCCTGCACATATCGCATGATGAGCTATGAACCACTGGAGCAGCCC 668
                                                                                                                                                                               EE: Foley & Lardner 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                               Conservative 218; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                           5.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP 91 114 300.6
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MOLECULE TYPE:
PCT-US94-12883-3
                                                                                                                                                                                                                          Sequence 1, Application US/08342411A Patent No. 5639616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.5%;
                                                                                                                                                                                                    GENERAL INFORMATION:
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PCT-US94-12883-3
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SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
APPLICANT: LIAO, Shutsuny
APPLICANT: SONG, Ching
TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9412883 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               685 TCACCCCCAGGAGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAAT 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
STRANDEDNESS: 811
STRANDEDNESS: 811
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APPLICATION NUMBER:
FILING DATE: 10-NOV-
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 79-09:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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10-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 8
US-08-496-841C-137
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Best Local Similarity
""+ches 72; Conserva
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US-08-342-411A-1
                                                                                                                                                                                                                                                   Sequence 137, Application US/08496841C
PATENT NO. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, 1

CURRENT APPLICATION DATA:

ADDITION UNMARRE. ISC/08/742.411
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SEQUENCE CHARACTERISTICS:
LENGTH: 1898 base pair
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                685 TCACCCCCAGGAGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAAT 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08
FILING DATE: 18-NOY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (, 79-0924
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ADDRESSEE: Arnold, White & Durkee
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77210-4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                 TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (512) 418-300
TELEFAX: (713) 789-2679
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REFERENCE/DOCKET NUMBER: ARC
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
APPLICATION NUMBER: US/08/496,841C
                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                     CITY: New York
STATE: New York
                                                                                                              ZIP: 10022
                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houston
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                                                                                                                                                                 EE: Darby & Darby, PC
805 Third Avenue
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Pred. No. 0.017;
0; Mismatches 47; Indels '0
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TOPOLOGY: Ilnear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 137:
US-08-496-841C-137
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 753-6
INFORMATION FOR SEQ ID NO: 137
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                     COUNTRY:
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Local Similarity 48.8%;
Les 63; Conservative
                                                                                                    FILING DATE:
                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Paul F. Fehlner, Ph.D. REGISTRATION NUMBER: 35,135 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-Jun-1995
CLASSIFICATION: 
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTTWCGGNARNCACMCNNCNGGGRNGNGGNNTWANARTNAWANCCAAWAAATANNTNANT 2226
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                                                                                                                                                                                                                                         94111-4187
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: (212) 7:
                                                                                                                                                                                                                                                                       California
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                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                         GAVIN, Kimberly
VENTION: ORIGIN OF REPLICATION COMPLEX GENES
EQUENCES: 24
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KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                                                                                          MCNALLY, Francis J
LAURENSON, Patricia
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LI, Joachim J
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                                                                                                                  US/08/484,105
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              A-59032/DJB/RAO
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Pred. No. 0.027;
                                                                                                                                                   Version #1.30
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                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/484,106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 62; Conserve
            TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 494-87
TELEFAX: (415) 494-877
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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                                                                   REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEPAX: (415) 494-8771
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APPLICANT:
APPLICANT:
                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TITLE OF I
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LENGTH: 3214 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3179 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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LOCATION:
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CITY: San Francisco
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 ENGTH:
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4 Embarcadero Center,
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3214 base pairs
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220..2802
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FOSS, Margit
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KOBAYASHI, Ryuj
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCNALLY, Francis J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAURENSON, Patricia
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er, Suite 3400
                                                                                                                                                                                                                                                            Version #1.30
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RESULT 12
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; LOCATION: (50)...(1285)
US-09-336-643A-82
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES
TITLE OF INVENTION: PRODUCTS: II
                                                       Sequence 389, Application US/09385982
Patent No. 6262334
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US-09-336-643A-82
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Best Local Similarity
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; LOCATION:
US-08-484-106-17
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Patent No. 6395, ...
Patent No. 6395, ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NO. 6399761el Human Potassium Channels FILE REFERENCE: SEQ-15F
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Miller, Andrew P. APPLICANT: Curran, Mark Edward
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                               FEATURE
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                                                                                                                                PPLICANT:
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Local Similarity 65.3%;
nes 62; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
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Wang, Jian-Wang
                                                                                                                                                                                                                                             Conservative
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Marc
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                                                                                                                                                                                                                                                         5.2%;
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Pred. No. 0.061;
""" amatches 33;
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Pred. No. 0.06;
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           AND GENE EXPRESSION
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                                                                                                                                                                                                                                     Gaps
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RESULT 13
US-09-363-708-3
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GENERAL INFORMATION:
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                                                                                       TELEFAX: (312) 474-044.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 59.1%;
Matches 68; Conservative
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CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME/KEY: misc_feature
LOCATION: (1)...(629)
OTHER INFORMATION: n = A,T,C
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EARLIER FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schmandt, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                 STRANDEDNESS:
TOPOLOGY: 11
                                                        LENGTH: 2246 Dase |
TYPE: nucleic acid
                                                                                                                                                                   NAME: Clough, David W.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                  FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 CACCATGATGTGAANAGTTTCNCAAATCTTTCAAAATNAAAAGTAATGACTTAGAAACTG 60
                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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: Illinois
                   TYPE:
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60606-6402
                                                                          2246 base pairs
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233 South Wacker Drive/6300 Sears
                                                                                                                       (312) 474-0448
                                 linear
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   /desc =
                   CDNA
                                              single
                                                                                                                                      474-6300
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"mouse PAL cDNA"
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Pred. No. 0.042;
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; LOCATION: 1.7859
; OTHER INFORMATION: /note= "sequence of plasmid pSW6"
US-07-854-596B-4
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                                                                                                              Matches
                                                                                                                         Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                     5644 AAAAAAAAAAAAAAAAAAAA 5663
                                                                                                                                                                                                                         FEATURE:
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APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 03-JUN-1992 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                      NAME: McDonnell, Jor
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                           AAAAAAAAAAAAAAAAAGAGA 792
                                                                               ATGCCTTTTATATATTATGTTTTTACTGAAATTAACTGAAAAATATGAAACCAAAAGTA 772
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52; Conservative
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                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                           7859 base pairs
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Pred. No. 0.13;
0; Mismatches 24;
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Search completed: March Job time: 76.7061 secs
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US-08-450-905B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 23-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9221587.0

FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, HOLLIE L.

REGISTRATION NUMBER: 31,321

REFERENCE/DOCKET NUMBER: 31,321
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 56; Conserv
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                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                              5644 AAAAAAAAAAAAAAAAAAA 5663
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 7859 base pairs
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APPLICATION NUMBER: (
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APPLICATION NUMBER: 07/982,759
FILING DATE: 08-MAR-1993
                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                          773
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: 617-526-5000
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                                                                               ATGCCTTTTATATATTATGTTTTTTACTGAAATTAACTGAAAAAATATGAAACCAAAAGTA 772
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Pred. No. 0.13;
0; Mismatches 24;
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Title: Perfect score: Sequence:

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Maximum Match 100%
Listing first 45 summaries
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rived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                 2003, 20:56:58; Search time 74.3669 Seconds (without alignments) 9222.973 Million cell updates/sec
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                                                               0 US-09-864-864-309
US-10-123-049-173
US-10-123-044-173
US-10-123-904-173
US-10-175-746-173
US-10-176-918-173
US-10-176-918-173
US-10-176-921-173
US-10-176-921-173
US-10-140-474-173
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                               Sequence 309, A
Sequence 173, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                            APPLICANT: Fling, Steve F.
APPLICANT: Mannion, Jane
APPLICANT: Menson, Darin R.
APPLICANT: Genson, Darin R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
CURRENT APPLICATION UNDMER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 309
LENGTH: 814
TYPE: DNA
ORGANISM: Homo sapiens
US-09-864-864-309

GALLS: Score 750.4; DB 10; Length 8
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US-09-864-864-309
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Patent No. US20020102679A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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                                                                      GACCAAAGGTGGAGCAACCCCGTTACCCTAAARATGAAAGGCTGGGGTTGGCTGGCCCTG 130
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Dillon, Davin C.
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Pred. No. 2.3e
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10 US-09-954-456-779
10 US-09-980-107-1335
10 US-09-880-107-1336
10 US-09-880-107-1334
10 US-09-880-107-1334
2 US-09-809-391-130
2 US-09-809-391-130
2 US-09-803-377-105
2 US-10-914-846-128
2 US-09-764-846-128
2 US-09-764-873-12
2 US-09-960-352-4144
2 US-09-960-352-4144
3 US-10-218-631-39
2 US-10-218-631-39
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Result No.

NO.

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                                                                                        GENERAL INFORMATION:
APPLICANT: Baker, Key
APPLICANT: Beresini,
APPLICANT: DeForge,
APPLICANT: DeForge,
APPLICANT: Desnoyers
APPLICANT: Geo, Wei-
APPLICANT: Goodward,
APPLICANT: Goddard,
APPLICANT: Goddward,
APPLICANT: Godowski,
APPLICANT: Godowski,
APPLICANT: Godowski,
APPLICANT: Sherwood,
APPLICANT: Stewart,
APPLICANT: Tumas,
APPLICANT: Tumas,
APPLICANT: Watanabe,
APPLICANT: Wood, Will
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APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
                                                                                                                                                                                                                                                                                       Sequence 173, A Publication No.
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Goddard, Audrey
Goddwski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Watanabe, Colin !
Wood, William
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Filvaroff, Ellen
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OR APPLICATION NUMBER: 60/063127
OR APPLICATION NUMBER: 60/063229
OR APPLICATION NUMBER: 60/06329
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/06329
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063550
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OR APPLICATION NUMBER: 60/064248
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OR APPLICATION NUMBER: 60/064248
OR FILING DATE: 1997-11-07
OR APPLICATION NUMBER: 60/06426
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/066364
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OR APPLICATION NUMBER: 60/059263
OR FILING DATE: 1997-09-18
OR APPLICATION NUMBER: 60/059352
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/059588
OR FILING DATE: 1997-09-24
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062285
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062287
OR APPLICATION NUMBER: 60/062814
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OR APPLICATION NUMBER: 60/062816
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OR APPLICATION NUMBER: 60/063045
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RR APPLICATION NUMBER: 60/05
DR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 1998-02-04

APPLICATION NUMBER: 60/C FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/C FILING DATE: 1998-02-09

60/074092 60/074086 60/073612 60/072320 60/069694 60/069334

APPLICATION NUMBER: 60/077791 FILING DATE: 1998-03-12

NR APPLICATION NUMBER: 60, NR FILING DATE: 1997-12-11 NR APPLICATION NUMBER: 60, NR FILING DATE: 1997-12-16 NR APPLICATION NUMBER: 60, NR APPLICATION NUMBER

OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-02-27
OR APPLICATION NUMBER: 60/079728
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/080165

APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081818 FILING DATE: 1998-04-15

APPLICATION NUMBER: 60/081695 FILING DATE: 1998-04-14

APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09

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OR APPLICATION NUMBER: 60/088858
OR FILING DATE: 19/98-06-11
OR APPLICATION NUMBER: 60/089532
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089599
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OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/090349
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OR FILING DATE: 1998-06-23
CTTTGTGACCATGCCCTGCACATATCGCATGATGAGCTATGAACCACTGGAGCAGCCCAC
                  AGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATT
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-01
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FILING DATE: 1998-06-24
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1; Mismatches
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OOR APPLICATION NUMBER: 60/085704
OOR FILING DATE: 1998-05-15
OOR APPLICATION NUMBER: 60/086414
OOR FILING DATE: 1998-05-22
OOR APPLICATION NUMBER: 60/086430
OOR FILING DATE: 1998-05-22
OOR APPLICATION NUMBER: 60/087106
OOR FILING DATE: 1998-05-28
OOR FILING DATE: 1998-05-28
OOR APPLICATION NUMBER: 60/088026
OOR FILING DATE: 1998-06-04
OOR APPLICATION NUMBER: 60/088730
OOR APPLICATION NUMBER: 60/088741

989 550 929 490 869 430 809 370 749 310 689 250 629

OR APPLICATION NUMBER: 60/08299
OR FILING DATE: 1998-04-24
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083545
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APPLICANT: Beresini, Mauree
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timochy
APPLICANT: Stewart, Timochy
APPLICANT: Tumas, Daniel
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Best Local Similarity
Matches 753; Conserv
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APPLICANT:
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SEQ ID NO 173
LENGTH: 1210
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CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stevart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
Wood, William
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Goddard, Audrey
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llarity 98.9%;
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Pred. No. 5.6e-200;
1; Mismatches 7;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
  Query Match
Best Local Similarity
Matches 753; Conserv
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APPLICANT:
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                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/123,904 CURRENT FILING DATE: 2002-04-16
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   Conservative
            93.0%;
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 Score 749.4; DB 9;
Pred. No. 5.6e-200;
1; Mismatches 7;
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RESULT 5
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         INVENTIÓN: SECRETED AND
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Wattanabe, Colin K
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Gerritsen, Mary E.
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Filvaroff, Ellen
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      TRANSMEMBRANE POLYPEPTIDES
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Application US/10175746 o. US20030027270A1
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; TITLE OF INVENTION: ACIDS ENCODING THE FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,47
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 173
; EEQ ID NO 173
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-173
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Pred. No. 5.6e-200;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333ORIC353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
FENTME: 1330
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           GAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAGAT
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Baker, Kevin
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
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Pred. No. 5.6e-200;
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; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 173
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; LENGTH: 1210
; TYPE: DNA
; ORGANISM: HOMO Sapien
US-10-176-918-173
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Best Local Similarity
Matches 753; Conserv
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333ORIC382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Filvaroff, Ellen
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Pred. No. 5.6e-200;
1; Mismatches 7;
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RESULT 8
US-10-176-921-173
; Sequence 173, App.
; Publication No. 1
                                                           ; TYPE: DNA
; ORGANISM: HOMO
US-10-176-921-173
                 Query Match
Best Local Similarity
Matches 753; Conserv
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APPLICANT: Beresini, Mau
APPLICANT: Desnoyers, Lu
APPLICANT: Desnoyers, Lu
APPLICANT: Esnoyers, Lu
APPLICANT: Go, Wei - Qian
APPLICANT: Goddard, Audr
APPLICANT: Goddwski, Pau
APPLICANT: Gurney, Austi
APPLICANT: Sherwood, Ste
APPLICANT: Sherwood, Ste
APPLICANT: Stewart, Timo
                                                                                          CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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APPLICANT:
APPLICANT:
                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRATITLE OF INVENTION: ACIDS ENCODING FILE REFERENCE: 93330R1C288
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Godowski, Paul J.
Gurney, Austin L.
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Wood,William
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b. US20030027276A1
                  Conservative
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              Score 749.4;
Pred. No. 5.6e
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US-10-137-865-173
VS-quence 173; Applica
PUBLICATION NO. US200;
GENERAL INFORMATION:
APPLICANT: Beker, Key
APPLICANT: Beresini
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Goddowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
         Stewart, Timothy A. Tumas, Daniel
                                                                                                                           Beresini, Maureen
DeForge, Laura
 Watanabe
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o. US20030032155A1
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POL
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POL
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330RIC154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wraf
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
ORGANISM: Homo Sapien
US-10-137-865-173
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Local Similarity 98.9%;
Les 753; Conservative
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                                                                                                                       CTTTGTGACCATGCCCTGCACATATCGCATGATGAGCTATGAACCACTGGAGCAGCCGAC
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                                                                       ACTGGCTTGATGGATCACCCCCAGGAGGGGAAAATGGTGGCAATGCCTTTTATATTAT
                                                                                                                                                    GAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAGAT
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Pred. No. 5.6e
1; Mismatches
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66-200;
es 7;
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APPLICANT: Baker, Kev
APPLICANT: Beresini
APPLICANT: DeForge,
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Best Local Similarity 98.9%;
Matches 753; Conservative
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APPLICANT:
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AGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATT 550
                                      GGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATATT
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RESULT

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLY

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C162

CURRENT APPLICATION NUMBER: US/10/140,474

CURRENT FILING DATE: 2002-05-06

PTIOT APPLICATION TEMOVED - See Palm OT File Wrapi
NUMBER OF SEQ ID NOS: 550

SEQ ID NO 173

LENGTH: 1210

TYPE: DNA
ORGANISM: Homo Sapien

US-10-140-474-173
                                                                                                                                                                                                                                                                                                    CCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATG
                                                        GCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAG
                                                                                                                                                                                                  CTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGA 190
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Pred. No. 5.6e
1; Mismatches
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US-10-142-431-173
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Best Local S
Matches 753
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330RIC251
CURRENT APPLICATION NUMBER: US/10/142,431
CURRENT FILING DATE: 2002-05-10
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             GCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAG 250
                                                     CTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGA 190
GCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCCAAGAAG
                                                                                                              GACCAAAGGTGGAGCAACCCCGTTACCCTAAARATGAAAGGCTGGGGTTGGGTGGCCCTG 130
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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b. US20030036179A1
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Pred. No. 5.6e-200;
1; Mismatches 7;
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; TYPE: DNA
; ORGANISM: Homo
US-10-143-114-173
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SEQ ID NO 173
LENGTH: 1210
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                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C211
CURRENT APPLICATION NUMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
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                                                     Prior Application removed NUMBER OF SEQ ID NOS: 550
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Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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          Sapien
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                                                               See Palm or File Wrapper
                                                                                                                     NUCLEIC
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RESULT 13
US-10-140-002-173
Sequence 173, Application US/1014(
Publication No. US20030037623A1
GENERAL INFORMATION:
APPLICANT Barceini, Maureen
APPLICANT Beresini, Maureen
APPLICANT DEFOYGE, Laura
APPLICANT DEFOYGE, Laura
APPLICANT Filvaroff, Ellen
APPLICANT Geno, Wei-Olang
APPLICANT Goo, Wei-Olang
APPLICANT Goodward, Audrey
APPLICANT Godowski, Paul J
APPLICANT Gurney, Austin L.
APPLICANT Gurney, Austin L.
APPLICANT Sherwood Steven
APPLICANT Sherwood Steven
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FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
ORGANISM: Homo Sapien
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nes 753; Conservative
 GAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAGAT
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                                           ACTGGCTTGATGGATCACCCCCAGGAGGGGAAAATGGTGGCAATGCCTTTTATATATTAT
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Wood, William
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Pred. No. 5.6e
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US-10-142-419-173
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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CURRENT FILING DATE: 2002-05-10
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APPLICANT: Beresini, Ma
APPLICANT: DeForge, Lau
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Similarity 98.9%;
53; Conservative
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Godowski, Paul J.
Gurney, Austin L.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Pred. No. 5.6e-200;
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CURRENT FILING DATE: 2002-04-15
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Gurney, Austin L.
Sherwood, Steven
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Wood, William
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source
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutaleostom1;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 1117)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/OTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM1968 row: c column: 07

High quality sequence stop: 709.

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CTCTGGTGGATGAACTAGAATGGGAAATTGCCCCAGGTGGACCCCAAGAAGACCATTCAGA
              CTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCATTCAGA 260
                                                                             CCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGG
                                                                                                                                          GGAGCAACCCCGTTACCCTAAARATGAAAGGCTGGGGTTGGCCTGCCTTCTGGGGG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLNAL1666 row: 1 column: 01 High quality sequence stop: 730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                               Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                     88.6%;
                                                                                                                                                                                                                                                   Score 714.2; DB 13; Pred. No. 5.3e-116; 1; Mismatches 19;
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BQ421069.1 GI:21116384
EST.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANd13197 row: d column: 14
High quality sequence stop: 542.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae;
1 (bases 1 to 868)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:609949"
/clone_lib="NIH_MGC_68"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6;
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Ното
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Pred. No. 7.6e-116;
1; Mismatches 37;
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880 AGEMCORT_7801623 NIH_MGC_72 5', mRNA sequence. BQ421827

Ното

sapiens mRNA

cDNA clone linear

EST 23-MAY-2002 IMAGE:6050568

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                      CCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATG
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AGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATT
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EST.
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Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, Mammalian
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1 (bases 1 to 880)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: sKin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: sKin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
Technologies."
38 a 208 c 256 g 176 t 2 others
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96.8%;
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Pred. No. 1.8e-114;
1; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11474 row: j column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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1 (bases 1 to 875)
         226
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Location/Qualifiers
/note="Organ: pooled colon, kidney, stomach: Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen), Research Genetics tracking code 023. Note: this is a NIH_MCC Library."
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                                                                                                                                                                                                                                            /clone="IMAGE:5189862"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                 /lab_host="DH10B"
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Sutheria; Primates; Catarrhini; Hominidae;
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                                                        mRNA sequence.
BI550162
BI550162.1 GI:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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603193045F1 NIH_MGC_95
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97.3%;
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Pred. No. 2.7e-113;
1; Mismatches 15;
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TCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMILEGE row: 1 column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 7
                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                         /note-*Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag); Oligo-dT primed using primer 5-TTTTTTTTTTTTTTTTVN-3', Size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NYMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.*

a 178 c 226 g 163 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5264339"
/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="hippocampus"
/lab_host="DH10B"
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Pred. No. 2.8e-112;
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 CTGAAATTA - - CTGACAAATTTGAAACCAAAAGTGAAAACAAAAAAA 766
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG824549
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602728454F1 NIH_MGC_15 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLCM1737 row: k column: 13
High quality sequence stop: 740.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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                                                              Similarity
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                                                                                                           /note=*Organ: colon; Vector: POTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)*

a 184 c 233 g 144 t 1 others
                                                                                                                                                                                                                           /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4868100"
                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_15"
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; Pred. No. 2.2e
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2e-109;
es 11;
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                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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602014708F1 NCI_CGAP_Brn64 Hc
5', mRNA sequence
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BF344334
found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM9413 row: p column: 01
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:4130512"
/clone="IMAGE:4130512"
/clone="IMAGE:4130512"
/clone="Ib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: NotI
/note="Organ: pcMV-SPORT6; Site_1: NotI
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: NotI
/note="Organ: pcMV-SPORT6; Site_1: NotI
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TGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGA 368
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                     GGCTGGGGCCAAAGTGAAAGTCCAGCGGTCTGCCAGCGCTTGGGCCACGGCGGCGGCCCT 68
                                                               TGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGA
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM11470 row: 1 column: 12
High quality sequence stop: 775.
Location/Qualifiers
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National Institutes of Health, Mammalian
Unpublished (1999)
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Tissue Procurement: Life Technologies, Inc.
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
/clone="IMAGE:5188307"
/clone=11b="NIH_MGC_116"
/lab_host="DH10B"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2461 row: c column: 06
High quality sequence start: 208
High quality sequence stop: 350.
Location/Qualifiers
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5', mRNA sequence.
BQ668530
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1 (bases 1 to 673)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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               196
          /clone_lib="NMAGE.6276413"
/clone_lib="NIH_MGC_102"
/clone_lib="NIH_MGC_102"
/tlssue_type="epidermoid carcinoma, cell line"
/lab_host="DilOB (phage-resistant)"
/note="Organ: sallvary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTGACCGGATGAAGGAGTATGGGGAACAGATTGATCCTTCCACCCATCGCAAGAACTA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGGGGAAATTGCCCAGGT 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGGTGGAGGTGCCTTATGCCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGAT
                                                                                                                                          mRNA sequence.
BI909759
BI909759.1 GI:
                                                                  Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 720)
                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                          BI909759
603070841F1 NIH_MGC_118
                                                                                                                                EST
                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                        Homo sapiens
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  cgapbs-r@mail.nih.
Procurement: Life
                                                                                                                                                                                                                                                 673
                                                                                                                                           GI:16173041
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99.7%;
                                                                                Chordata;
Primates;
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Pred. No. 3.5e
0; Mismatches
                                                                                                                                                                           720 bp mRNA
Homo sapiens cDI
Technologies,
                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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.5e-108;
les 2;
                                                                                                                                                                             cDNA clone
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                                              Collection (MGC)
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IMAGE:5219603 5',
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                                                             AGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATT
                                                                                                       GGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATATT
                                                                                                                   GGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATATT
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1552 row: a column: 12
High quality sequence stop: 717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5219603"
/clone_lb="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Westor: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV /note="Westor: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.8%;
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Pred. No. 1.3
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                                                                                                                                                       GACCAAAGGTGGAGCAACCCCGTTAACATTAAARATGAAAGGCTGGGGTTGGCTGGCCCTG 130
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM798 row: b column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                     Similarity
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601589289F1
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                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: lung; Vector: pOTBF; Site_1: XhoI; Site_2: ECORI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 216 c 292 g 176 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:3943223"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (phage-resistant)"
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Pred. No. 6.5e-105;
1; Mismatches 48;
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                                                                                                                                                                                                                                            mRNA sequence.
BG704443
BG704443.1 GI
                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 791)
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602688633F1 NIH_MGC_95 Homo
                                        found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov
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           High quality sequence stop:
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4821008"
/clone_1bb="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
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  TACGTACGTGTAGTGGGCCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGA
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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/Lissue_type="neuroblastoma"
/Ibb_Most="DHJOB (phage-resistant)"
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National Institutes of Health, M
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Clone distribution: MGC clone distribution information can be

Clone distribution: MGC clone distribution information can be
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                          182
             /lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRJ/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 180 c 237 g 146 t
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/clone_lib="NIH_MGC_7"
/tlssue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
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Search completed: March 30, 2003, 20:56:44
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SUMMARIES

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ALIGNMENTS

RESULT 1 AAZ38326

AAZ38326 standard; cDNA; 546 BP

AAZ38326;

09-FEB-2000 (first entry)

Human transmembrane protein cDNA clone HP10390 coding sequence

HP10390; transmembrane domain; stomach cancer cell; antibody; assay reagent; diagnostic marker; primer; probe; antisense; g agonist; antagonist; ligand; therapeutic; ds. gene therapy;

Homo sapiens

Location/Qualifiers
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03-JUL-1997;
03-JUL-1997;
19-MAY-1998;
19-MAY-1998;
17-JUN-1998;
This cDNA clone encodes human secretory peptide-9, or 2sig9, variant (see AAW88474). Zsig9 (see also AAW88469) is overexprofuman brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors. Thus, Zsig can be used as an indicator for cancer. Zsig9 cDNA was discovered in a placenta clone from a full-term pregnancy cDNA library which contained a expressed sequence tag (see AAX06971). The invention provides
                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides (see AAX06968-70) encoding Zsig9 polypeptides (see AAX08469-77) including mature polypeptides, other processed forms, variants and mouse orthologues. The Zsig9 gene, or probes derived from it, can be used to determine if Zsig9 gene, or probes derived rom it, can be used as diagnostic agents to determine the presence of Zsig9 can be used as diagnostic agents to determine the presence of Zsig9, and thus the presence of cancer. They can also be labelled with radioisotopes or fused with toxins and used to treat tumours which overexpress Zsig9. Antisense nucleotides derived from Zsig9 cDNA can also be used to inhibit the growth of tumour cells. Zsig9 proteins can be used to enhance the growth or development of the placenta, heart or liver.
           07-FEB-2000
                                     AAZ08293;
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                                                                                                                                 protein-9, zsig9 that arises due to alternative splicing, allelic variation or silent mutations that result in amino acid changes. This sequence is mapped to the human chromosome 12q15 region. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to zsig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to zsig9 and it may be radiolabelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding zsig9. The zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma, etc., at an early stage.
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                           The present DNA sequence is a gene encoding the variant of the secretory
                                                                                                                                                                                                                                                                                                                       Disclosure; Page 33-35; 45pp; English.
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P-PSDB; AAY15135.
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                                           (SAGA )
(PROT-)
                             Kato
                                                                  28-APR-1998;
                                                                                                04-NOV-1999
                                                                                                                                                                                 assay reagent; diagnostic marker; primer;
agonist; antagonist; ligand; therapeutic;
      WPI; 2000-023358/02.
P-PSDB; AAY52391.
                                                                                 27-APR-1999;
                                                                                                               WO9955862-A2.
                                                                                                                                                                   Homo
                                                                                                                                                                                                 HP10390; transmembrane domain; stomach cancer cell;
                                                                                                                                                                                                              Human transmembrane protein
                                                                                                                                                                                                                               09-FEB-2000
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                                           SAGAMI CHEM RES CENT PROTEGENE INC.
                             Kimura T;
                                                                                                                                                                                                                                                            standard; cDNA; 814
                                                                                                                                                                                                                              (first entry)
                                                                  98JP-0119395
                                                                                 99WO-JP02226
                                                                                                                             /*tag= a
/product=
                                                                                                                                            Location/Qualifiers
145..693
                                                                                                                             "Human transmembrane protein HP10390"
                                                                                                                                                                                                              cDNA clone HP10390
                                                                                                                                                                                 probe; antisense; ds.
                                                                                                                                                                                                 antibody;
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Human proteins with transmembrane domains, involved in control of cell proliferation and differentiation, useful for treating e.g. cancer or inflammation –
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Claim 4; Page 106-107; 114pp; English.

This sequence represents the human cDNA clone HP10390 which encodes a 20 kD protein with one putative transmembrane domain in the N-terminus. The cDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically.

Sequence 814 BP; 210 A; 194 C; 241 G; 169 T; 0 other;

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

2.53e-103 960.00 100.00% 100.00% 100.00% 21

Length:
Matches:
Conservative:
Mismatches:
Indels:

814 182 0 0

Gaps:

Alignment Scores: Pred. No.: Score:

	181 GluLeu 182 685 GAGCTA 690	68	Qy Qy	
180	161 ASPLYSLEUCYSSETLYSATGThrASPLEUCYSASPHISALBLEUHISILESETHISASP	6;	ρ δ δ	
160 624	141 ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys	5(pb qq	
140 564	121 GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle	5 1:	D Qy	
120 504	101 HisarglysasnTyrValargValValGlyargasnGlyGluSerSerGluLeuaspLeu 	4 1	D Q	
100	81 LeuLeuGluGluIleCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr 	<u>u</u> _	Db Qy	
80 384	61 ASPGlySerGlnSerValValGluValProTyrAlBArgSerGluAlaHisLeuThrGlu 	ω _	p Qq	
60 324	41 GluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro 	2	D Qy	
40 264	21 ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp 	2	D _b	
204	1 MetLysGlyTrpGlyTrpLeuAlaLeuLeuGlyAlaLeuLeuGlyThrAlaTrpAla	ř.	D Q	
	US-10-082-502-17 (1-182) x AAZ38327 (1-814)	-10-0	US	

RESULT 5
ABK52765
ID ABK5

ABK52765 standard;

CDNA;

814

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Score:
  Percent Similarity:
                                                                                   The invention relates to modulators of a cancer-related genes. Also described are: (1) processes for identifying an anti-neoplastic agents comprising contacting a cell exhibiting neoplastic activity with a compound first identified as a cancer related gene modulator, and detecting a decrease in the neoplastic activity. (2) a process for determining the cancerous state of a cell by determining an increase in the level of expression of at least one gene, where an elevated expression relative to a known non-cancerous cell indicates a cancerous state or potentially cancerous state. The anti-neoplastic agent is useful for treating cancer or for protecting an animal against cancer. The immunogenic composition is also useful for treating cancer in an animal, where the composition elicits the production of cytotoxic T lymphocytes specific for the immunogenic composition. Preferably, the animal is a human. The cancer-linked genes and polypeptides are also useful as targets for cancer therapy or chemotherapy. The present sequence represents a cancer-linked gene located on chromosome 12, which encodes transmembrane protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2000;
12-OCT-2000;
12-OCT-2000;
12-OCT-2000;
16-OCT-2000;
19-OCT-2000;
19-OCT-2000;
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P-PSDB;
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                                                               Sequence 814
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11-OCT-2000;
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DB; AAU97063.
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2000US-239802P.
2000US-239805P.
2000US-239806P.
2000US-241682P.
2000US-241733P.
2000US-241932P.
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/product= "Transmemb
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24-JUL-2000;
24-AUG-2000;
                                     24-JUL-2001; 2001WO-JP06371
                                                                                        WO200208416-A1
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                        Antibody; antigen;
                                                                                                                                                                                                                                Nucleotide sequence of human polypeptide HP10390
                                                                                                                                                                                                                                                           11-JUN-2002
                                                                                                                                                                                                                                                                                    ABL41995;
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2000JP-0222743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           method comprises inoculating an antibod of antibody preparation. The a fusion protein having an antigen protein fused to the C-terminal side (extracellular) of a transmembrane domain protein (the N-terminal side of which is intracellular), and then isolating and purifying the antibody from the animal. The antibodies can be used as drugs, vaccines, diagnostic reagents and laboratory reagents. The present sequence encodes a polypeptide, designated Hp10390, which was used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody preparation by inoculation of an animal with a vector expressing a fusion protein of an antigen on the C-terminal side transmembrane domain for use as drugs, diagnostic reagents and
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ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
                                                                           LeuLeuGluGluIleCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr 100
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                                                                                                                   CATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTA
                                       GTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAA
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DB; ABB09717.
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Best Local S. Query Match: DB:
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ABK09772
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13-JUN-2000;
21-JUN-2000;
03-AUG-2000;
01-MAR-2001;
                                                                                                                    and for treating ovarian cancer in a patient. An antigen presenting cell that expresses the sequences is useful for treating ovarian cancer by incubating CD4+ and/or CD8+ T cells isolated from a patient. The T cells can then be proliferated and administered to the patient to inhibit the development of cancer. The DNA sequences are useful as probes or primers for nucleic acid hybridisation, to direct expression of a polypeptide in appropriate host cells. Detecting the presence of a cancer in a patient involves obtaining a biological sample from the patient, contacting the biological sample with an agent that binds to the protein, detecting the amount of protein that binds to the agent, comparing the amount of protein that binds to the agent, comparing the presence of cancer. Sequences ABK09464-ABK09802 represent PCR primers and CDNA molecules encoding ovarian tumour proteins of the invention.
                                                                                                                                                                                                                                                                                                        The
                                                                                                                                                                                                                                                                      polypeptide comprising a portion of an ovarian tumour protein. The sequences of the invention are useful for stimulating an immune reand for treating ovarian cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                              Xu J,
Algate
                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide ovarian tumour protein, use human ovarian cancer
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                                                                                                                                                                                                                                                                                                                                Claim 1; Page 253-254;
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PA, Fling SP,
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2000US-211457P.
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Mannion J,
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                          12-SEP-1997;
01-JUL-1997;
01-JUL-1997;
12-SEP-1997;
                                                                           30-JUN-1998;
                                                                                                                                                    Human; secreted protein; gene therapy; protein therapy; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; autoLimmune disease; AIDS; developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; schizophrenia; immunological disorder; mood disorder immune deficiency disease; respiratory disorder; arthritis; skeletal; haematopoietic disorder; neural; osteoporosis; metabolic disorders; cardiovascular; endocrine; gastrointestinal; asthma; diagnosis; ds.
         (HUMA-) HUMAN
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                                                                                                                                    Homo sapiens
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        GENOME SCI INC
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97US-0051480.
97US-0058598.
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CC The invention relates to nucleic acid sequences (AAX22111 to AAX22134) CC encoding human secreted proteins (AAY01135 to AAY01138). The secreted CC protein gene sequences are deposited with the ATCC under deposit number CC ATCC 209118. Host cells comprising recombinant vectors containing the CC acid sequences are used for the recombinant production of the CC secreted proteins. The polynucleotide and amino acid sequences are useful CC conditions e.g. by protein or gene therapy. Pathological conditions can CC sample or by determining the amount of the new polypeptides in a CC polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed CC in, and include developing products for the diagnosis or treatment of CC cancer, tumours, developmental abnormalities and foetal deficiencies, autoimune diseases, lymphomas, Alzheimer's and cognitive disorders, cancer, fumours, developmental abnormalities and foetal deficiencies, cancer, tumours, developmental abnormalities and foetal deficiencies, CC schizophrenia, immunological disorders, immune deficiency diseases. CC (AIDS), mood disorders, respiratory disorders, atthritis, asthma, CC osteoporosis, metabolic disorders, cardiovascular disorders, endoorine contentifying their binding partners. The polypeptides are also useful gene encoding a human secreted protein (see descriptor line for gene and clone identification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and the secreted polypeptides they encode -useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, immune deficiency diseases or blood disorders
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Sequence 1180 BP; 258 A; 304 Ç 363 Ģ; 250 Ξ, 5 other,

US-10-082-502-17 (1-182) x AAX22112 (1-1180)	Pred. No. Scores: Score: Score: Percent Similarity: Best Local Similarity: Query Match: DB:
) x AAX22112	4.16e-103 960.00 100.00% 100.00% 100.00% 20
(1-1180)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
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20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
30-DEC-1900;
06-JAN-2000;
11-FEB-2000;
11-FEB-2000;
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02-DEC-1999;
09-DEC-1999;
                Baker KP,
Gerritsen
Smith V,
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breast; prostate; ce
cartilage; ear; prol
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 WPI; 2001-408281/43
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                  Stewart
                         Beresini M,
ME, Goddard
                                                                   99WO-US28301

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99WO-US30095

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2000WO-US30993

2000WO-US30991

2000WO-US30991

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2000WO-US034341

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2000WO-US04414

2000WO-US04914

2000WO-US05001
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CC AAS21244-AAS21518 encode for novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CPRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC molecules involved in binding interactions. The polynucleotides encoding CC PRO polypeptides can be used to generate probes, antisense RNA/DNA, creations of the process of the process of the process of the process of the proposities can be used to generate probes, antisense RNA/DNA, creating the process of the proposities can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lung,
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Sequence 1210 ВP; 261 A; 316 C; 379 ດ 254 Ŧ, 0 other;

Percent Similarity:
Best Local Similarity:
Query Match: US-10-082-502-17 (1-182) x AAS21330 Score: Alignment Scores: Pred. No.: 4.31e-103 960.00 100.008 100.008 100.008 22 (1-1210) Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1210 182 0 0

Ş 밁 Ş 543 21 سر ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp

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AAX97884
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PR 117-
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13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
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diagnostic, roic
also include d
                                                                                                                                                                                                                                                                         AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAY36129-Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.
                                                                                                                                                                                                        No.:
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98US-0081563.
98US-0096116.
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03-JUL-1997;
03-JUL-1997;
03-JUL-1997;
19-MAY-1998;
19-MAY-1998;
17-JUN-1998;
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           (ZYMO ) ZYMOGENETICS
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Mouse secretory peptide-9 (Zsig9) orthologue cDNA
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                                                                                                                                                                                                                                             peptide-9; 2sig9;
herapy; diagnosis;
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                98US-0099005.
97US-0051704.
97US-0888088.
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358..417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA clone encodes novel mouse secretory peptide-9, or Zsig9 (See AAW88476), an orthologue of novel human Zsig9 (see AAW88469). CC Human Zsig9 is overexpressed in a number of tumours including CC brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid CC and lymphoma tumors, and thus can be used as an indicator for CC cancer. The invention provides polynucleotides (see AAX06968-70) cc encoding Zsig9 polypeptides (see AAW88469-77) including mature polypeptides, other processed forms, variants and the mouse orthologues. The Zsig9 gene, or probes derived from it, can be contrologues. The Zsig9 gene, or probes derived from it, can be cused to determine if Zsig9 is present on chromosome 10, and if a mutation has occurred. Antibodies raised against Zsig9 can be cused as diagnostic agents to determine the presence of Zsig9, and thus the presence of cancer. They can also be labelled with cradioisotopes or fused with toxins and used to treat tumours which overexpress Zsig9. Antisense nucleotides derived from Zsig9 con Connections can also be used to enhance the growth or development of the proteins can be used to enhance the growth or development of the proteins can be used to enhance the growth or development of the
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P-PSDB; AAW88476.
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                                                     GluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
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                                                       The present DNA sequence is an ortholog encoding the secretory protein-9, zsig9 derived from mouse. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to Zsig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to zsig9 and it may be radio-labelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of Zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding Zsig9. The zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma etc., at an early stage.
                                   Sequence 1069
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nucleotides
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                                                                                                                                                                                             Disclosure; Page 37-38; 45pp; English.
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                                                                                                                                                                                                                    tumors using antibodies, antagonists and es to secretory protein-9 (Zsig9)
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/product- "Mouse Zsig9 secretory |
/note- "Overexpressed in tumours"
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AC ABR36
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                                                                                                                                                                                                                           Human secreted protein; hyperproliferative disorder; autoimmune disorder; Immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
  06-APR-2000; 2000US-195605P
                                                                                              18-OCT-2001
                                                                                                                                         WO200177289-A2
                                                                                                                                                                                                                                                                                                                                                                          cDNA sequence
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                                             29-MAR-2001; 2001WO-US10232.
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(GEMY) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C; Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG; Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR; WPI; 2002-179322/23.

Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders

Claim 1; Page 297; 393pp; English.

The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. haemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK3623 represent the cDNA sequences of the invention that encode for novel human constitutions.

Sequence 657 BP; 177 A; 149 C; 185 G; 146 T; 0 other;

DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
24	95.21%	97.75%	98.88%	914.00	4.86e-98	
Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
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US-10-082-502-17 (1-182) x ABK36007 (1-657)

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	В	1 GGTTGGCTGGCTTGCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAG	AACCGCCTGGGCTCGGAGGAGCCAG 60	
	Qy	25	pGluLeuGluTrpGluIleAlaGln 44	
	Ъ	61 GATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGGGGAAATTGCCCAC	GAACTAGAATGGGAAATTGCCCAC 120	
	Qy	45 \	eArgIleAsnProAspGlySerGln 64	
	Вb	121 GTGGACCCCAAGAAGACCATGCAGATGGGATCTTTCCGGATCAATCCAGATTGCAGCCAG	CCGGATCAATCCAGATTGCAGCCAG 180	
	Qy	65	aHisLeuThrGluLeuLeuGluGlu 84	
	당	181 TCAGTGGTGGAGGTGCCCTATGCCCGCTCAGAGGCCCACATCACAGAGCTGCTGGAGGAG	CCACATCACAGAGCTGCTGGAGGAG 240	
	Q	85 IleCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsn	eAspProSerThrHisArgLysAsn 104	
	Db	241	TGATCCTTCCACCCATCGCAAGAAC 300	
	Qy	105 T	rGluLeuAspLeuGlnGlyIleArg 124	
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	Q	125 IleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIleValGluGluTyr 144	aCysGluSerIleValGluGluTyr 144	
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13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
                                                                                   Local Similarity:
                                                                                                                                                                AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAY36129-Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.
                                                                                                                                                                                                                                           Example 28; Page 194-195;
                                                                                                                                                                                                                                                            Extended cDNAs encoding secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX97837
                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic;
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  21
                           MetLysGlyTrpGlyTrpLeuAlaLeuLeuGlyAlaLeuLeuGlyThrAlaTrpAla
ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGlu-LeuGluTr
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DB; AAY36153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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                                                        (1-182) x AAX97837 (1-832)
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97US-0066677.
97US-0069957.
98US-0074121.
98US-0081563.
98US-0096116.
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                                                                                                                                                 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; cytostatic; thrombotic; osteopathic; forensic;
therapy; chromosome mapping; secretion vector; ss.
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97.84%
97.30%
94.90%
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Conservative:
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RESULT 15
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                                                                                                                                                                                                                      Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; expressed sequence tag; sEST; probe; chemotactic; proliferative; immunomodulatory; haematopoletic; chemotinetic; analyssic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antiinflammatory; cytostatic; antipacterial; antipactingal; antiviral; antiinflammatory; cytostatic; vulnerary; antiparkinsonian; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antiviral; antidabetic; neuroprotective; notropic; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmane disorder; multiple sclerosis; allergic condition; insulin dependent disorder; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                       15-OCT-1999;
                                                                                                                       20-APR-2000
                           (GEMY ) GENETICS INST
                                                           15-0CT-1998;
                                                                                                                                                    WO200021991-A1
                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                 tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uGlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLys-PheAlaCysGluSerI 140
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                                                                                                                                                                                                                 infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed sequence tag SEQ ID
                                                           98US-0104436
                                                                                         99WO-US24206
                                                                                                                                                                                                               depression;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC Chemoktactic; proliferative; immunomodulatory; haemattopoletic; cc chemoktactic; proliferative; immunomodulatory; haemattopoletic; cc chemoktactic; antibacterial; antifungal; antifutal; antifulatic; cc cytostatic; antibacterial; antifungal; antifutal; antifulatic; cc antiasthmatic; ulinerary; antifulatic; osteopathic; neuroprotective; cc antisthmatic; uniterary; antifulatic; osteopathic; neuroprotective; cc anticonvulsant; and antifulation; antipsoriatic; cerebroprotective; cc anticonvulsant; and antifulation of full-length cDNAs and genomic DNA complexity and in vaccines. The sergs are useful as probes for the cc identification and isolation of full-length cDNAs and genomic DNA cc molecules which correspond to the sergs. Proteins encoded by the sergs are useful in assays for determining biological activity and raising cc multiple sclerosis, insulin dependent diabetes), allergic conditions cc (asthma), myeloid or lymphold cell deficiencies, wounds, burns, ulcers, casteoporosis, osteoarthritis, central nervous system disorders (Alzhelmer's, Parkinson's, Huntington's disease, stroke), coagulation cd disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's or steoporosis, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given the sempolitication of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags (SESTs), isolated from human, mouse, chicken and rat
tissue sources. The SESTs can have a range of activities depending on
the tissues they were isolated from. The activities include:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 228-229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                104
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                                                                                                                                     uLeuLeuGluGluIleCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerTh 100
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Search completed: March 30, 2003, 22:42:53 Job time: 145.849 secs

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1: /cgn2_6/ptodata/
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Match
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Xgapop 10.0 , 1

Ygapop 10.0 , 1

Fgapop 6.0 , 1

Delop 6.0 , 1
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-09-163-285-1

US-09-724-864-14

US-09-724-87-073-10

US-08-257-073-10

US-08-961-083-159

US-08-961-527-208

US-08-961-527-208

US-09-071-035-3

US-09-071-035-1

US-08-750-1528-1
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    Sequence 3, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 16, Appl
Sequence 15, Appl
Sequence 208, Appl
Sequence 208, Appl
Sequence 1, Appli
                                                                                                                                                    Description
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                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09163285;
Patent No. 6204013
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 P.
TITLE OF INVENTION: AND USES THER
NUMBER OF SEQUENCES; 4
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/090,39

FILING DATE: June 24, 1998

ATTORNEY/AGENT INFORMATION:

NAME: MANDIAGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI--

TELECOMMUNICATION INFORMATION:

TELEPAN: (617)742-4214

INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-163-285-3
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                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           STREET: 28 St
CITY: Boston
STATE: Massac
                                                                                                                               APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                COUNTRY:
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28 State Street
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VENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
VENTION: AND USES THEREOF
                                                                                                                                                                                                                                               USA
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4, 1998
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US-08-993-380-3
US-08-938-105-2
US-09-131-8318-2
US-09-131-8318-1
US-09-069-637-1
US-09-322-360-1
US-09-106-637-2
US-09-106-637-2
US-09-106-637-2
US-09-102-433-1
US-09-102-433-1
US-09-102-433-1
US-09-102-433-1
US-09-103-1558-47
US-08-485-3558-49
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US-08-885-93-18
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Best Local Similarity:
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                                      GENERAL INFORMATION:
APPLICANT: Khodadoust
TITLE OF INVENTION: N
TITLE OF INVENTION: A
NUMBER OF SEQUENCES:
                                                                                                           Sequence 1, Application US/09163285 Patent No. 6204013
                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
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STRANDEDNESS: single
TOPOLOGY: 14----
 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AspGluLeuGluTrpGluIleAlaGlnValAsp---ProLysLysThrIleGlnMetGly
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               ADDRESSEE:
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                                                                                                                                                                                                                                    AlaCysGluSerIleValGluGluTyrGluAspGluLeuIleGlu---PhePheSerArg
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                                                                                                                                                                                 CAGGAGCAGCCCCTACAAAATTTTCTCTGT 552
                                                                                                                                                                                                                                                                                         CTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCCAGCGTGGAGGTCACATACCTCAAGAAG
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                                                                                                                                                                                                                                                                                                                                                              GlyGluSerSerGlu-------LeuAspLeuGlnGlyIleArgIleAsp 126
                                                                                                                                                                                                                                                                                                                                                                                                                             GlnIleAspProSerThrHis-----ArgLysAsnTyrValArgValValGlyArgAsn 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGACAAGGCTGGAAGAGCCTTAGAGAATTTATGTGAGCGGATCCTGGACTAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerPheArgIleAsnProAspGlySerGlnSerValValGluValProTyrAlaArgSer 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGAGCTACAGGCGGAACTGAGTCGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGGG
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28 State Street
                                                                                Khodadoust, Mehran
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                                                   NOVEL MSP-5 PROTEIN AND USES THEREOF
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            & COCKFIELD,
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Matches:
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PRIOR APPLICATION NUMBER: 60/090,398

FILING DATE: June 24, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-049

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1512 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: FEATURE:
467
                                                                                                                                                                                                                                                                                                                                                                                                                                   371
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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GGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGGTGAAGGTGGAT
                                  GlyGluSerSerGlu-----
                                                                                                    GlnIleAspProSerThrHis-----ArgLysAsnTyrValArgValValGlyArgAsn 112
                                                                                                                                            GAGACAAGGCTGGAAGAGGCCTTAGAGAATTTATGTGAGCGGATCCTGGACTAT----- 424
                                                                                                                                                                          GluAlaHisLeuThrGluLeuLeuGluGluIleCysAspArgMetLysGluTyrGlyGlu
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                                                                                                                                                                                                                                                                                                                            AspGluLeuGluTrpGluIleAlaGlnValAsp---ProLysLysThrIleGlnMetGly 54
                                                                                                                                                                                                                                                                                          ACAGAGCTACAGGCGGAACTGAGTCGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGGG 319
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                                                                    -----AGTGTTCACGCTGAGCGCAAGGGCTCACTGAGATATGCC-----AAG 466
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                                -----LeuAspLeuGlnGlyIleArgIleAsp 126
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DB:
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; ORGANISM: Mouse
US-09-724-864-14
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US-09-724-864-14
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CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. NO. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Murison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.105001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                     26 LeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaGlnVal
                                                                                                                                                                                                                                                                                                                                                       98 TCGGCTTCGGCTCCCACACTGGATGATGAAGAGAAGTACTCGGCTCATATGCCGGCTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LeuAl&LeuLeuGly-----AlaLeuLeuGlyThrAlaTrpAlaArgArgSer---
     IleAspSerAspIleSerGly--
                              CAGATGAAGCGTCTCACGGGCCCAGGACTTAGCAAGGGGGCCAGAG------CCAAGA 391
                                                             TyrValArgValValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArg 124
                                                                                                                        CysAspArg---MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsn 104
                                                                                                                                                                                       ValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluIle
                                                                                                                                                                                                                        GAGGCTAAATCTCAC-----GGA 250
                                                                                                                                                                                                                                                        AspProLysLysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSer
                                                                                                                                                                                                                                                                                      CTGCGCTGCGATGCCTGCCGGGCTGTGGCCTTCCAGATGGGGCAACGTCTGGCGAAAGCA
                                                                                                  TGCTCTCAGAACTGGCAGTCCTATGGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCCAGCGTGGAGGTCACATACCTCAAGAAG 586
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24.51%
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----ThrLeuLysPheAlaCysGluSer 139
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                                                                                               -----GTTCATGAAGTGAAC 340
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US-10-082-502-17 (1-182) x US-09-453-702B-62 (1-61663)
                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                  ; MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID US-09-453-702B-62
                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 62:
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                                                                                                                                                                                                                                                                                                                                                NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch.
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ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney S
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 61663
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TITLE OF INVENTION: No. 6365723el Sequences of
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blattner, Frederick R.
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                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Dec-1999 CLASSIFICATION: <Unknown>
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STATE: WI
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-257-073-10
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                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 11-JUN-1993
                        ATTORNEY/AGENT INFORMATION:
                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                     APPLICATION NUMBER: FILING DATE: 18-MAR
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                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/257,073 FILING DATE: 09-JUN-1994
                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCGGGGACGCTGAAATCTCCTGATGGTGAGGCGATATCAGGAGCAAATATTACCCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Curtis, Morris & Safford, P.C. 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -CGCAGTCTTGTTGAGGTTAGCATACCCGGAGAACTGCTGACAGATTTCCG
                                                                                               NUMBER: US 07/852,305
                                              20-MAR-1991
                                                              US 07/672,183
                                                                                                                                                                            US 08/075,783
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US-08-961-083-159
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US-08-257-073-10
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                                                                                                                                                                                                                 Sequence 159, Application US/08961083 Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                     1597 TTTAATAATATTTTGACAAAGATGTCGTAGATAAAATATTCAGTGCAAGA 1647
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REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION IMPORMATION:
TELEPHONE: (212) 840-333
                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1492 AAAAAAATTAATCAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1432 GATAATAAGGAAAGAAAAATATTCATTAATAACATTAAAAAAACAAATTGATTTAGAAGAA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1372 TCATATGGTGATTTAATGAATCCTGATACTAAAGAAAAAATTAATGAAAAAATTATTACA 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1312 GTATATCCTTTACCACTCACTGATATTCATAATTCATTAGCTGCAGATAATGATAAAAAT 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1252 AAATCACAAGATCCTACGAAATCTGTTCAAATACCAAAAGTTCCTTATCCAAATGGTATT 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5181 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 IleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIleValGlu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 ArgAsnGlyGlu-------SerSerGluLeuAspLeuGlnGly 122
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                                                                                                                                                                                                                                                                                                                                                                                             156 AlaAspAsn-----
                                                                             CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 AspGluLeuGluTrpGluIleAlaGlnValAspProLysLysThrIleGlnMetGlySer 55
                                        ZIP: 20850
                                                      COUNTRY:
                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 AlaHis-----LeuThrGluLeuLeuGluGluIleCys-----AspArgMetLys 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 PheArgIleAsnProAspGlySerGlnSerValValGluValProTyrAlaArgSerGlu 75
                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                               9410 Key West Avenue
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85.00
43.31%
22.93%
8.85%
                                                                                                                                                                              Streptococcus pneumoniae Antigens : 452
3.50 inch,
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Matches:
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Indels:
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  1.4Mb
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US

SOFTWARE:

ASCII Text

MSDOS version

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS vei

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Best Local Similarity:
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REFERENCE/DOCKET NUMBER: 9834
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
     941
                                      160
                                                                                                                                                                126 AspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIleValGluGluTyrGlu 145
                                                                                                         146
                                                                                                                                        851 CAAAATAAAGTTGCTGATTTA-
                                                                                                                                                                                                   791 CAGGATGAATTAGATAAAGAAGCAGAAGAAGCTGAGTTGGATAAAAAAGCTGATGAACTT 850
                                                                                                                                                                                                                                                                      731 GCAAAAAACAACAGAACTTGAAAAACTTCTTGACAGCCTTGATCCTGAAGGTAAGACT 790
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APPLICATION NUMBER:
                                                                                                                                                                                                                           106 ValArgValValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIle 125
                                                                                                                                                                                                                                                                                                                                        671 GTTATAGAAGCTAAATTAAAAAAAGGAGAAGCTGAGCTAAACGCTAAACAAGCTGAGTTA 730
                                                                                                                                                                                                                                                                                                                                                                                                          620 GATAATTTGAAAAAACTTCTTGCTGGTGCG------GATCCTGATGATGGCACAGAA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               560 AAACTTCAATATGAAATTTCTACTTTGGAACAAGAAGTTGCTACTGCTCAACATCAAGTA
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                                                                                                                                                                                                                                                                                                     86 CysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyr 105
                                                                                                                                                                                                                                                                                                                                                                         66 ValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluIle
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                               LysaspLysLeuCysSerLysargThraspLeu 170
                                                              ATTAGTAACCTTGAAATATTACTTGGAGGGGCTGATNCTGAAGATGATACTGCTGCTCTT
                                                                                             AspGluLeuIleGluPhePheSerArgGluAlaAspAsn-------val 159
CAAAATAAATTAGCTACTAAAAAAGCTGAATTG 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAla-------GlnVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AspProLysLysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSer
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84.00
40.35%
21.64%
8.75%
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Matches:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
917 CAGGATGAATTAGATAAAGAAGCAGAAGAAGCTGAAGTTGGATGAAAAAAAGCTGATGAACTT 976
                                106 ValArgValValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIle 125
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                   746 GATAATTTGAAAAAACTTCTTGCTGGTGCG-----GATCCTGATGATGGCACAGAA 796
                                                                                                                                                                                                                                                                                          686 AAACTTCAATATGAAATTTCTACTTTGGAACAAGAAGTTGCTACTGCTCAACATCAAGTA 745
                                                                                                                                                                                                                                                                                                                                                                 626 GCAACTCTAAAGGTAGCACTAGCGAAGAAAGAAGTAGAGGCTAAGGAACTTGAAATTGAA 685
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                                                                                                                                                                              66 ValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluIle 85
                                                                                                                                                                                                                                                      46 AspProLysLysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSer 65
                                                                                                                                                                                                                                                                                                                         30 AlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAla------GlnVal 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
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                                                                                                       CysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyr 105
                                                                                                                                            GTTATAGAAGCTAAATTAAAAAAAGGAGAAGCTGAGCTAAAACGCTAAACAAGCTGAGTTA 856
                                                                     GCAAAAAAACAAACAGAACTTGAAAAACTTCTTGACAGCCTTGATCCTGAAGGTAAGACT 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20850
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Matches:
Conservative:
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Indels:
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                                                                                                                 US-10-082-502-17 (1-182) x US-09-071-035-3 (1-1216)
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Best Local Similarity:
Query Match:
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Patent No. 6448043
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                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1007
                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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   278
                                                            260
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                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: A. Anders Brookes REGISTRATION NUMBER: 36
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                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII Text
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GCACAAGATGAAATGTTAGTGGACTTAAAACCATATATGGATGATGACACAATCGGCTGG 337
                          SerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGlu-----LeuGluTrp 40
                                                        GGCTGGTTATGGAATGCT-----
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US-09-071-035-1
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APPLICANT: G11 H.
                                                                                                                                                                  TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
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                                                                                                                                                                                                                               NAME: A. Anders Brookes REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                 STRANDEDNESS:
                                                                                                                TYPE:
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                                                                              TOPOLOGY:
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US-08-750-152A-1
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       APPLICANT: NAKAMATSÜ, TSÜYÖSHI
TITLE OF INVERVION: ALPHA-KETOGLUTARATE DEHYDROGENASE GENE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                 COUNTRY:
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                                                                     APPLICATION NUMBER: FILING DATE:
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KIMURA, EIICHIRO
ABE, CHIZU
KAWAHARA, YOSHIO
                                                                                                                                                                                                                                                   OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 703-413-300
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
   3008 GGCATCACCGGCTCCCAGAAGCTTCCACACGGCCTTGAGACCAACATCTCCCGTGAAGAG
                                                                        2951
                                                                                                                            2900 CTCTCCAACGAA-----GATGCAGAAGCAGTCGTCCGCGACTTCCACGACCAGATG
                                                                                                                                                                                                   2849
                                                                                                                                                                                                                                                                2789
                                                                                                                                                                                                                                                                                                                                                                                         2669
                                                                                                                                                                                                                                                                                                                2729 TACCGTCGTCGCTTCGGCAAGGACGTCTTCATCGACCTCGTTTGCTACCGCCTCCGCGGC 2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: FEATURE:
                                       169 AspLeu-----
                                                                                                        149
                                                                                                                                                   129 IleSerGlyThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeu 148
                                                                                                                                                                                                                   111 ArgAsnGlyGluSerSerGluLeu-----AspLeuGlnGlyIleArgIleAspSerAsp 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: FEATURE:
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REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                              92
                                                                                                                                                                                                                                                                                                                                                                                                         56 PheArgIleAsnProAspGlySerGlnSerValValGluValProTyrAlaArgSerGlu 75
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                                                                                                                                                                                                                                                                                                                                                           76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Brevibacterium lactofermetum STRAIN: ATCC13869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                             GAATCTGTGTTCAACGAAGTCAAGGAAGGCGGCAAG---AAGCAGGCTGAGGCACAGACC
                                                                                                                                                                                                                                                                                                                                      AlaHis-----LeuThrGluLeuLeuGluGluIleCysAspArgMetLysGlu
                                                                                         IleGluPhePheSerArgGluAlaAspAsnValLysAspLysLeuCysSerLysArgThr 168
                                                                                                                                                                                                                                                   CACAACGAAGCTGATGATCCTTCCATGACCCAGCCAAAGATGTATGAGCTCATCACCGGC 2848
                                                                                                                                                                                                                                                                        TyrGlyGluGlnIleAspProSer---ThrHisArgLysAsnTyrValArgValValGly 110
                                                                                                                                                                                                                                                                                                                                                                             TTCCACGTCAATGGTGATGACCCAGAGGCAGTTGTCTGGGTTGGCCAGCTGGCAACCGAG
                                                                                                                                                                                       CGCGAGACCGTTCGTGCTCAGTACACCGAAGACCTGCTCGGA-----CGTGGAGAC
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443..4213
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421..428
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4243..4281
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281..287
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81.50
43.97%
25.53%
8.49%
                             -CysAspHisAlaLeu-----HisIleSerHisAspGlu 181
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Indels:
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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/99/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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Best Local Similarity:
Query Match:
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US-09-103-840A-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4382013 TATGCCGCCCGCATCGAC---GCGGTGCAT------
                                                                                                                                                                                                                                                                                                       4382133 GTTATTCGCGCCCAGCAGCTCCCGGAGGCGGGCTGATCGAGTCGGCGTTTGCTGACGCG 4382074
                                                                                                                                                                                                                                                                                                                                                                                  4382193 CGCAGCGCGGCACGCAGTTCGCGCTGACTGAGATTCAGTCGACGGCGGGGCCGATGGGC 4382134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FLETSCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                              4382073 TACGCCAGCACCACCGCTGTCGTGGGCCAATGCCAGCTGGCGGCCCCAGCTAGACGCC 4382014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3068
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                 132 ThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeu------ 148
                                                                                                            112 AsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAspIleSerGly 131
                                                                                                                                                                                         92 TyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgValValGlyArg 111
                                                                                                                                                                                                                                                                  75 GluAlaHisLeuThrGluLeuLeu------GluGluIleCysAspArgMetLysGlu
                                                                                                                                                                                                                                                                                                                                       55 SerPheArgIleAsnProAspGlySerGlnSerValValGluValProTyrAlaArgSer 74
                                                                                                                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 --- ArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp 40
---ATCAAAGAGGTGTGGGAGTTTCTGACCGACCAGGACGAAGACGAGATCCAGCGCATC 4381882
                                                                          -----GCGGCGGTCCTGGATTTGTTGGCC---CGCATCTGCGATCCGCTGACCGGG 4381939
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81.50
39.90%
22.80%
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Indels:
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Matches:
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APPLICANT: FRASER, Claire M.

APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

ITILE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

ITITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 7

SEQ ID NO 1
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Best Local Similarity:
Query Match:
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 4381881 GCCCATGACATCGCGGTGGTGGTCGACCAGTTCAGCGGGGAAGTG----
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4389700 ---ATCAAAGAGGTGTGGGAGTTTCTGACCGACCAGGACGAAGACGAGATCCAGCGCATC 4389644
                                                                                                                                                                                                                                                                                                                                                     4389895 GTTATTCGCGCCCAGCAGCTCCCGGAGGCGGGGCTGATCGAGTCGGCGTTTGCTGACGCG 4389836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4389994 GGGGATTCGACAAAGCTACGTGCGGCGCT--------
                                132 ThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeu------
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                                                                                                                                                                                                                                                                                                              75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAspIleSerGly 131
                                                                                                                                                                                                                  TyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgValValGlyArg 111
                                                                                                                                                                                                                                                                                                       GluAlaHisLeuThrGluLeuLeu------GluGluIleCysAspArgMetLysGlu
                                                                                  -GCGGCGGTCCTGGATTTGTTGGCC---CGCATCTGCGATCCGCTGACCGGG 4389701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GluIleAlaGlnValAspProLysLysThrIle---GlnMetGly 54
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81.50
39.90%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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                                                            US-10-082-502-17 (1-182) x US-08-837-029-1 (1-833)
                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                            Score:
                                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-837-029-1
                                                                                                                 Query Match:
                                                                                                                                                                                       Alignment Scores:
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Patent No. 5945303
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4389595 GCGTTGGCTGCGGAGATCACCGCGGTGGTGTCGCACGCC 4389557
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                                                                                                                                                                            No . :
                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic sold
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             FEATURE:
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REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: We1 et al.
TITLE OF INVENTION: Human Hematopoietic -
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
            63
                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                            7 LeuAlaLeuLeuGlyAlaLeu------LeuGly-----
                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 LysLeuCysSerLysArgThrAspLeuCysAspHisAla 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
CTGCTGCTGCTGGGAGCCTGGGCCATCCCAGGGGGCCTCGGGGACAGGGCGCCACTC 122
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108..608
                                                                                                                                                                                                                                                                              sig_peptide
42..107
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Matches:
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CURRENT APPLICATION NUMBER: US/08/993,380B
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens (modified)
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                                               US-10-082-502-17 (1-182) x US-08-993-380-3 (1-1173)
                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                               Alignment Scores:
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US-08-993-380-3
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APPLICANT: Sh1, Qinwei
APPLICANT: Song, Qian-Li
TITLE OF INVENTION: SINGLE CHAIN POLYPEPTIDES COMPRISING TROPONIN I AND
TITLE OF INVENTION: TROPONIN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08993380B Patent No. 6077676
10 LeuLeuGlyAlaLeuLeuGlyThrAlaTrpAlaArgArgSerGlnAspLeuH1sCysGly 29
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Patent NO. 6353151
GENERAL INFORMATION:
APPLICANT: Leinwand, Leslie A.
APPLICANT: Vikstrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                            ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1000 GACAAAAATGCTGATGGCTACATCGAC 1026
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                         CLASSIFICATION:
                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                          COUNTRY:
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Best Local Similarity:
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3085 CTCAAGAAGAAAGAGTTTGACATCAGTCAGCAGAACAGTAAAATAGAGGACGAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 GluLeuGluTrpGluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5661 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 ThrAlaTrpAlaArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                             GluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLysAspLys 162
                                                                                                                               GAGCGAGCAAAGCCGGAAGCTGGAGGTGACCTGAAGCTGACCCAGGAGAGCATCATGGAC
                                                                                                                                                                                                                                                                               GlnIleAspProSerThrHisArgLysAsnTyrValArgValValGlyArgAsnGlyGlu 114
::::::::: ||| ||| ||||
                                                                                                                                                                                                                                                                                                                           AAGAAAGCTCTTCAAGAGGCCCACCAGCAAGCCCTAGATGACCTTCAGGCTGAGGAAGAC
                                LeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisIleSerHisAspGlu 181
                                                                                                                                                             Asp------IleSerGlyThrLeuLysPheAlaCysGluSerIleValGlu 142
                                                                                                                                                                                                                              SerSerGluLeuAspLeuGlnGly-------IleArgIleAspSer 127
                                                                                                                                                                                                                                                             AAGGTCAACACTGACC-----AAGTCTAAAGTCAAGCTG-----
                                                                                                                                                                                                                                                                                                                                                          GluAlaHisLeuThrGluLeuCeuGluGluIleCysAspArgMetLysGluTyrGlyGlu 94
                                                                                                                                                                                                                                                                                                                                                                                          AAAAACCTGACAGAGGAGATGGCCGGGCTGGACGAGATCATTGCCAAGCTGACCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                          ArgIleAsnProAspGlySerGlnSerValValGluVal-----ProTyrAlaArgSer 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGGCCAAGAAGCGCAAGCTGGAAGAC---GAGTGCTCAGAGCTCAAGAAAGATATCGAT
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Search completed: March Job time: 1662.68 secs 31, 2003, 04:04:16

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Result
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-DB-Published_Applications_NA .QFMT_fastap_SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-USI0082502_CGGN_1 1145_grunat_24032003_135103_6870
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MAAP -LARGEQUERY -NGE_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model -DEV=xlp
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Maximum Match 100%
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1: /cgn2_6/ptodata/2/pubpna/[
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11: /cgn2_6/ptodata/2/pubpna,
12: /cgn2_6/ptodata/2/pubpna,
13: /cgn2_6/ptodata/2/pubpna,
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14: /cgn2_6/ptodata/2/pubpna,
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                                                                                                                                                                                                                                                                                                                   . /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
. /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
. /cgn2_6/ptodata/2/pubpna/US06_REW_PUB.seq:*
. /cgn2_6/ptodata/2/pubpna/US06_EUBCOMB.seq:*
. /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
. /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
. /cgn2_6/ptodata/2/pubpna/US08_REW_PUB.seq:*
. /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
. /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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                  10 US-09-864-864-309
9 US-10-028-072-173
9 US-10-121-049-173
9 US-10-123-904-173
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         Sequence 309, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
                                                                                                     Description
APPLICANT: HOUSE, MALLING, Paul A.

APPLICANT: Eling, Steve P.

APPLICANT: Hangon, Jame R.

APPLICANT: Mannion, Jame R.

APPLICANT: Menson, Darin R.

APPLICANT: Carter, Darink

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

ITILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.523

CURRENT APPLICATION NUMBER: US/09/864,864

CURRENT FILING DATE: 2001-05-23

NUMBER OF SEQ ID NOS: 341

SOFTWARE: Corixa Invention Disclosure Database

SEQ ID NO 309

LENGTH: 814

TYPE: DNA

ORGANISM: Homo saplens
           US-09-864-864-309
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APPLICANT:
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APPLICANT: Mitcham, Jens
APPLICANT: Harlocker, St
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US-10-176-482-479
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US-10-176-918-173
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Sequence 173, App Sequence 174, App Sequence 278, App Sequence 479, App Sequence 479

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Percent Similarity:
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                                                                                                                   Sequence 173, Applica Publication No. US200 GENERAL INFORMATION:
APPLICANT Baker, Key APPLICANT Beresini APPLICANT DeForge, APPLICANT Filvarof APPLICANT Gao, Weight APPLICANT Gao, Weight APPLICANT Gao, Weight APPLICANT Geodard, APPLICANT Godowski APPLICANT Godowski
                                                                                                                                                                                                                                                                                          RESULT 2
US-10-028-072-173
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Desnoyers, Luc
Filvaroff, Ellen
                    Wood, William
                                 Tumas, Daniel
Watanabe, Colin K
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OR APPLICATION NUMBER: 60/065186
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OR APPLICATION NUMBER: 60/065846
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OR APPLICATION NUMBER: 60/066453
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OR APPLICATION NUMBER: 60/074086
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NUMBER: 60/085704: 1998-05-15

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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/0

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APPLICANT: Beresini, Mauree
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gorvitsen, Mary
APPLICANT: Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 173
LENGTH: 1210
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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Desnoyers, Luc
Filvaroff, Ellen
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Percent Similarity:
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US-10-123-904-173
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US-10-123-904-173
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
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APPLICANT: Beresini, Maur
APPLICANT: DeForge, Laura
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                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C54
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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Gerritsen, Mary E.
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Filvaroff, Ellen
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TITLE OF INVENTION: ACLDS ENCODING THE SAM:
FITLE OF INVENTION: ACLDS ENCODING THE SAM:
FILE REFERENCE: P3330RLC160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File NUMBER OF SEQ ID NOS: 550
LENCTH: 1210
TYPE: DNA
                                       ; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Homo :
US-10-140-470-173
  Alignment Scores: Pred. No.:
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US-10-140-470-173
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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DeForge, Laura
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APPLICANT: Beresini, Mau
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APPLICANT: Desnoyers, Lu
APPLICANT: Desnoyers, Lu
APPLICANT: Gay, Wei-Qian
APPLICANT: Gerritsen, Ma
APPLICANT: Goddard, Audr
APPLICANT: Goddard, Audr
APPLICANT: Goddwski, Pau
APPLICANT: Gurney, Aust
APPLICANT: Sherwood, Ste
APPLICANT: Sherwood, Ste
APPLICANT: Stewart, Time
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                                  APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C353
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Wood, William
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RESULT 7
US-10-176-918-173
; Sequence 173, Applica
; Publication No. US200;
; GENERAL INFORMATION:
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US-10-175-746-173
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Goddard, Audrey
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 Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wel-Qiang
Gerritsen, Mary E.
Goddard, Audrey
                                                                                           Application US/10176918 o. US20030027275A1
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APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steeven
APPLICANT: Smith, Vittoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Thang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POL
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
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NUMBER OF SEQ ID NOS: 550
TYPE: DNA
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; ORGANISM: Homo Sapien
US-10-176-921-173
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APPLICANT:
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P333GRIC288

CURRENT APPLICATION NUMBER: US/10/176,921

CURRENT FILING DATE: 2002-06-20
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 ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
                                                                CATCGCAAGAACTACGTGCGTAGTGGGCCCGGAATGGAGAATCCAGTGAACTGGACCTA
                                                                            H1sArgLysAsnTyrValArgValValGlyArgAsnGlyGluSerSerGluLeuAspLeu 120
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Godowski, Paul J.
Gurney, Austin L.
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; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Homo :
US-10-137-865-173
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
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                                             AspGlySerGlnSerValValGluValProTyrAlaArgSerGluAlaHisLeuThrGlu
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary E.
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Filvaroff, Ellen
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CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C162
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
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SEQ ID NO 173
FENGTH: 1210
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                                                                                                                                                   APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C251 CURRENT APPLICATION NUMBER: US/10/142,431 CURRENT FILING DATE: 2002-05-10
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APPLICANT:
APPLICANT:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Desnoyers, Luc
Filvaroff, Ellen
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CURRENT FILING DATE:

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RESULT 12
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Best Local Similarity:
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APPLICANT:
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        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC211
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Watanabe, Colin K
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Gerritsen, Mary E.
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Filvaroff, Ellen
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NUMBER OF SEQ ID NOS: 550
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    Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
                                                             Baker, Kevin
                                             DeForge, Laura
                                                     Beresini, Maureen
                                                                            Application US/10140002 o. US20030037623A1
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US-10-140-002-173
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
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Sherwood, Steven
Smith, Victoria
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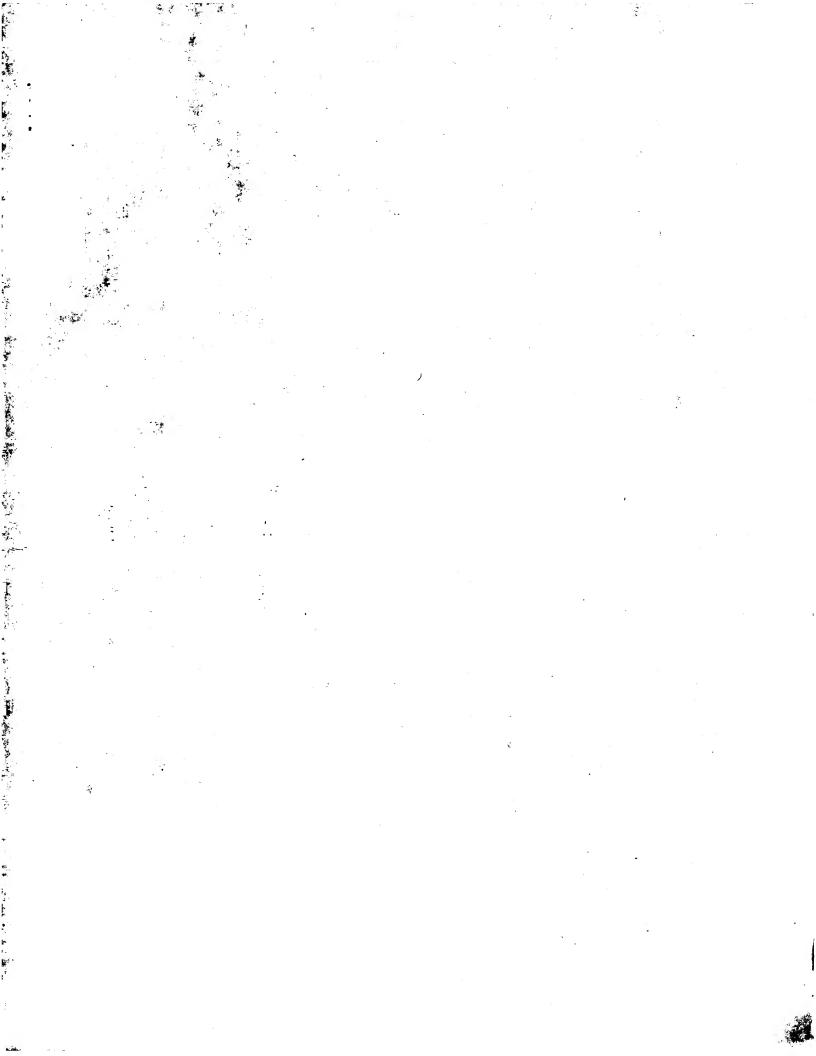
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C244
CURRENT APPLICATION NUMBER: US/10/142,419
CURRENT FILING DATE: 2002-05-10
Prior Apploication removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
TYPE: DNA
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APPLICANT: Baker, Kevin
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ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
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                                        CAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATT
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Stewart, Timothy A.
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Filvaroff, Ellen
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Best Local Similarity:
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LENGTH: 1210
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TITLE OF INVENTION: ACLDS ENCODING THE SAME
FILE REFERENCE: P9330R1038
CURRENT APPLICATION NUMBER: US/10/123,262
CURRENT FILING DATE: 2002-04-15
PILOT APPLICATION removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Gurney, Austin L.
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Watanabe, Colin K
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Search completed: March 31, 2003, 11:59:04
Job time: 58.0233 secs



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Minimum DB :
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-Q-/cgn2_1/USPTQ_spool/US10082502/runat_24032003_135100_6599/app_query.fasta_1.1308
-Q-/cgn2_1/USPTQ_spool/US10082502/runat_24032003_135100_6599/app_query.fasta_1.1308
-DEST -QEMT=fastap -SUFFIX-rst -MINMATCH=0.1 -LOOPELT=0 -LOOPEXT=0
-UNITS=blts -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITST=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10082502_GCGN_1 _15425_GTUNATCH=0 -MAXLEN=200000000
-USER-US10082502_GCGN_1 _15425_GTUNATCH=0 -MAXLEN-100GLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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ALIGNMENTS

AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BM832828	RESULT 1
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and	<pre>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 588)</pre>	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	human.	EST.	BM832828.1 GI:19189237	вм832828	5', mRNA sequence.	=	BM832828 588 bp mrNA linear EST 06-MAR-2002		

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                                                                                            CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGG
                                                                                                                                                                                      Korea Research Institute of Bioscience & Biotechnology 52 Ebeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409
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21C Frontier Korean EST Project 2001
Unpublished (2002)
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Location/Qualifiers
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Plate: 11 row: B column: 03
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Site_2: NotI; The poly (A)+ RNA was decapped with tabacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dT-selected
mRNA by priming with dT-tailed vector. The dT-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli ToplOF' by electroporation method.
After analyzing and sequencing about 2,000 - 3,000
colonies in original cDNA library, the abundant cDNAs were
selected and amplified by PCR reaction using vector region
primer including T7 promotor as 5 primer and N(dT)14 as
3 primer. The PCR products were used as template for
synthesis of biotinylated single stranded RNA by in vitro
transcription reaction. The synthesized RNA probes were
hybridized with antisense single stranded cDNAs prepared
from original liberary and incubated with avidin-gel.
After removing DNA-RNA hybrids by centrifuge, the
subtracted cDNA libraries were constructed by
transformation of the remaining DNA into competent cells E.
coli ToplOF' with electroporation method."
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Location/Qualifiers
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1 (bases 1 to 591)
Kim, N.S., Hahn, Y.,
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Plate: 11 row: H column: 01
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Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Research Center
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Site_2: NotI; The poly (A)+ RNA was decapped with tabacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
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first strand cDNA was synthesized from ollgo dT-selected
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vector was adjusted to have about 60nt. The cDNA vector
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US-10-082-502-17 (1-182) x BM832888 (1-591)
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                                                                  AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisIleSerHisAsp
                                                                                                                     ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
                                                                                                                                                                        GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle 140
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                                                                                                                                 CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGG
                                                                   ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp 40
GluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancress Consortium
Harvard University, Howard Hughes Medical Institute
Dept_of_Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI712899 611 bp mRNA linear EST 11-MAI 1d98f09.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5085832 5 similar to TR:Q9Y2B0 Q9Y2B0 TYPE II MEMBRANE PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dmelton@blohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing
Washington University Genome Sequencing Center For informati
obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 611)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -40RP from Gibco
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Size-selected on agarose gel. Average insert size -1kb. 5'
XhOI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692.**
a 143 c 184 g 127 t
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/clone="IMAGE:5085832"
/clone_lib="HR85 islet"
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/lab_host="DH10B"
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Mammalia; Eutheria;
1 (bases 1 to 697)
                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM9413 row: p column: 01 High quality sequence stop: 692.
                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Clone distribution: MGC clone distribution information can
                173
        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4150512"
/clone=lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 719)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
                                              Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                              BE733900
601568370F1 NIH_MGC_21
                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.G.E. Consortium (1 DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
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Location/Qualifiers
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/note="Organ: placenta; Vector: pOTB); Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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/tissue_type="choriocarcinoma"
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/db_xref="taxon:9606"
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Best Local Similarity:
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LeuLeuGluGluIleCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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/lab_host="DH10B (phage-resistant)"
/lab_host="DT97" colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 745)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. plate: LLCM79 row: k column: 22 High quality sequence stop: 739.
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
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601581586F1 NIH_MGC_7
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                                                                                  /lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRX/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 180 c 237 g 146 t
                                                                                                                                                                                                               /clone="IMAGE:3936141"
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
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Tissue Procurement: DCTD/DTP
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BM552907
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Contact: Robert Strausberg, Ph.D.
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM.968 row: C column: 07
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5', mRNA sequence.
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/lab_Nost="DHOB (phage-resistant)"
/note="Organ: skin; Vector: pOTB); Site_1: xhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
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Tissue Procurement: ATCC/DCTD/DTP
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6;
Site_2: Sall; Cloned unidirectionally. p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Miklos Paukovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; v
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 783)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                /note-*Organ: brain; Vector: pBluescriptR (modified pBluescript RS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Captrapper method (Carninci, in preparation). Library constructed by M. Brownstein (NUM/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 189 c 225 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5264328"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 868 by AGENCOURT_7911956 NIH_MGC_68 HG 5', mRNA sequence.
BQ421069 BQ421069.1 GI:21116384
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                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; V
Mammalla; Eutheria; Primates; Catarrhini;
1 (bases 1 to 868)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13197 row: d column: 14
                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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                                                                                                          quality sequence stop: !
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6009949"
/clone_lib="NIH_MGC_68"
/tissue_type="large_cel
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1 MetLysGlyTrpGlyTrpLeuAlaLeuLeuGlyAlaLeuLeuGlyThrAlaTrpAla

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Collection (MGC)

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                                                                                         mRNA sequence.
BG704443
BG704443.1 GI
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 791)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
203 c 257 g 168 t 8 others
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), S
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lini.gov
Plate: LLAM10727 row: a column: 09
High quality sequence stop: 785.
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/lab_host="DH10B"
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/clone_lib="NIH_MGC_95"
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), sh
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
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/tissue_type="hippocampus"
/lab_host="DH10B"
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            Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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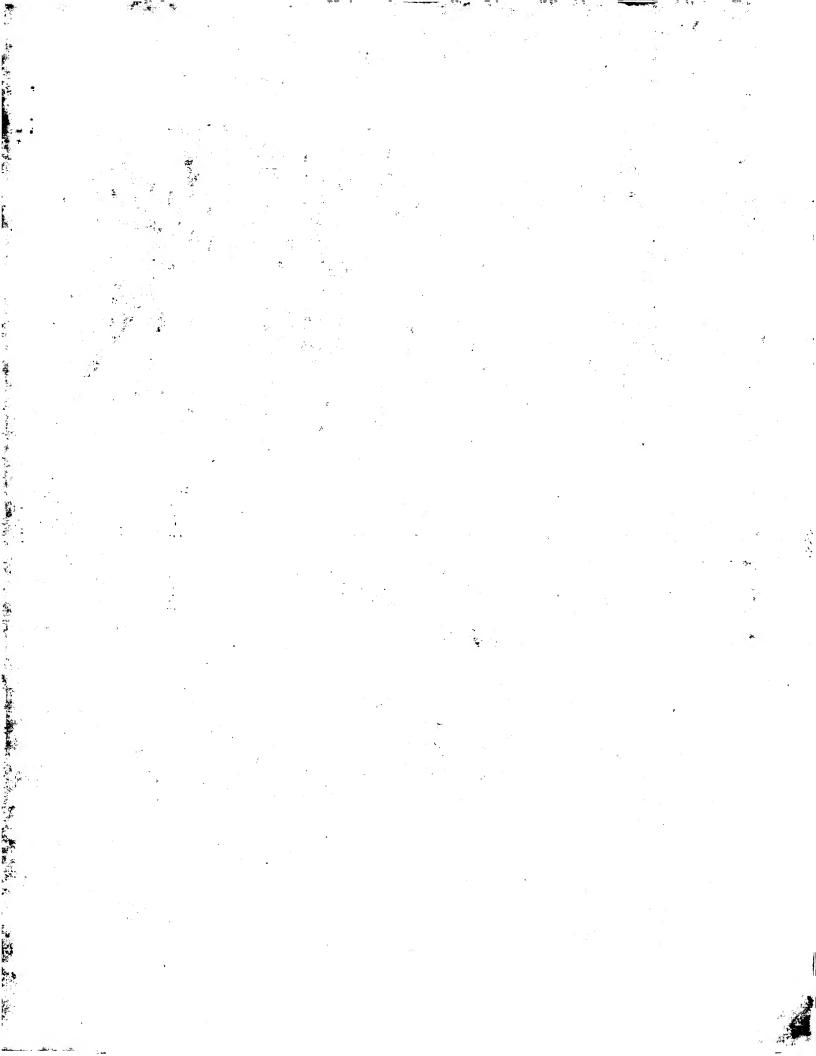
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  Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                  Functional
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Sciurognathi; Muridae;
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US-10-082-502-17 (1-182) x AK007914 (1-772)
                                                                                                           Best Local Similarity:
                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
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/strain="C57BL/6J"
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Search completed: March 31, 2003, 04:51:05 Job time: 1173.85 secs



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Command line parameters:

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Sequence 309
AX440456
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Lodes,M.J., Algate,P.A., Fling,S.
Carter,D.
                                                                                                                                                                                                                                                                                                                                                                                                                              Patent: WO 0190154-A 309 29-NOV-2001; CORIXA CORPORATION (US)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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/db_xref="taxon:9606"
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Benson, D.R.
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                                                                                                            ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
                                                GAAATTGCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCA
                                                                                                 CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGG
                                                                                                                                                 GAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-JUN-1998) Seishi Kato, Research Institute Rehabilitation Center for the Disabled, Department of Rehabilitation Engineering; 4-1 Namiki, Tokorozawa, Sait 359-8555, Japan (E-mail:seishi@rehab.go.jp, Tel:042-995-3100(ex.2568), Fax:042-995-3132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           perection of cDNAs encoding putative type II membrane the cell surface from a human full-length cDNA bank Gene 228 (1-2), 161-167 (1999)
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type II membrane protein.
type II membrane protein.
Homo sapiens gastric adenocarcinoma
clone_lib:pKA1-meta-1 clone:HP10390.
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/db_xref="taxon:9606"
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Olsson, P.-A. and Lindholm, D.
Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1080)
Bornhauser,B.C., Olsson,P.-A. and Lindholm,D.
NSAP is a novel saposin-like protein that interacts with MIR
stimulates neurite outgrowth
                                                                                                                                                                                                                                                        Submitted (13-APR-2001) Neuroscience, Husargatan 3, Uppsala 75123, Sweden
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/db_xref="taxon:9606"
/chromosome="12"
/map="12q15"
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1 269 c 343 9 230 t
                                                                                                                                                            /note="NSAP; encodes a type 2 membrane
putative ER retention motif"
/codon_start=1
                                                                                                                                /product="saposin-like protein"
/protein_id="AAK38148.1"
/db_xref="GI:20196199"
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AX464040
AX464040.1
                                                                                                                                                                                    Homo sapiens
Eukaryota; Me
Mammalia; Eut
                                                                                                                        Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.

Secreted, and transmembrane polypeptides and nucleic acids encoding.
                                                                                                 Genentech
                                                                                                         Patent:
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ch_Inc. (US)
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316 c 379 g 25
                                                                                     Location/Qualifiers
                                                                                                                                                                                  Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                MGC.
house mouse.
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Del
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                  Direct Submission
Submitted (22-MAY-2001) National Institutes of Headene Collection (MGC), Cancer Genomics Office, Nationatitute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                              Strausberg, R
                                                                                                                                                  Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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IMAGE:2650612,
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ne MGC:6853
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National Cancer
da, MD 20892-2590,
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US-10-082-502-17 (1-182) x BC008261 (1-798)
                                                ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
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GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle
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This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA g1: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.
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/db_xref="taxon:10090"
/map="129,C575L/63,FVB/N"
/clone="MGC:6853 IMAGE:2650612"
/tlssue_type="Mammary tumor. Brca
months old, gross tissue."
/clone_lib="NCI_CGAP_Mam3"
/lab_host="DH10B"
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/db_xref="GI:14198401"
/db_xref="GI:14198401"
/db_xref="LocusID:56530"
/translation="MKCWGWLALLLGYLLGTAWARRSQDLHCGACRALVDELEWEIAR
/translation="MKCWGWLALLLGYLLGTAWARRSQDLHCGACRALVDELEWEIAR
KNYVRYVSRNGSSELDLQGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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Sheppard, P., Jelinek, L., Whitmore, T., Blumberg, H., Lehner, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-SEP-1999) Biomolecular Informatics, ZymoGenetics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, USA
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/protein_id="AAF01433.1"
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            Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Balbrooks, S.L., Amaratunge, K., Bonnin, D., Bouck, J., Bowle, S., Bireva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Bireva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Bireva, M., Brown, E., Brown, M., Bryant, N.P., Buck, C., Chen, G., Chen, G., Chen, G., Chen, S., Chen, S., Chen, S., Chen, S., Chen, S., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Day, S., Dinh, H.H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hayles, M., Holloway, C., Hernandez, J., Howard, S., Huber, J., Hulyk, S., Hume, J., Jockson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jockson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joulah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Louiseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Martin, R., Martindale, A., Martinez, E., Massey, E., Miched, M.P., Meador, M., Martin, R., Martindale, A., Martinez, E., Massey, E., Miched, M.P., Meador, M., Marshahar F., Martinez, R., Martinez, R., Martinez, R., Martinez, R., Martinez, R., Marhahar F., Martinez, R., Martinez, R
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BASE COUNT
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                               Alignment Scores:
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      Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2001 this sequence version replaced gi:14547727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Consensus quality: 161278 bases at least Q40

Consensus quality: 170806 bases at least Q30

Consensus quality: 174843 bases at least Q20

Estimated insert size: 168803; sum-of-contigs estimation

Estimated insert size: 163288; agarose-fp estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

Quality coverage: 5.8x in Q20 bases; sum-of-contigs estimation
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Chemiatry: Dye-terminator Big Dye: 100% of reads
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Center code: BCM
Web Bite: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: HMKZ
Center clone name: RP11-764L14
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                                                                                                                                                                                                                                                                           1. .158198
                                                                                                                                                /chromosome="12"
/clone="RP11-764L14"
                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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6: gap of unknown length
6: contig of 41917 bp in length
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7: contig of 3064 bp in length
7: gap of unknown length
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys 160
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Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan,Rocha,S., Durbin,K.J.,
                                                                                                                                                                                                                                                     Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 155023)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Banbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Branch J., Bimage,K., Bankenburg,K., Bonnin,D., Benton,J., Bimage,K., Bankenburg,K., Bonnin,D., Branch J., Bimage,K., Bankenburg,K., 
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Homo sapiens chromosome 12 clone
SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homsi, F., Howard, S., Huber, J., Hulk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, 2., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Mahashwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Milner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Noser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nitchell, T., Mohabbat, K., Morgan, M., Morris, S., Nguyen, N., Nitchell, T., Mohabbat, K., Morgan, M., Morris, S., Nguyen, N., Nitchell, T., Mohabbat, K., Morgan, M., Morris, S., Nguyen, N., Nitchell, T., Mohabbat, K., Morgan, M., Morris, S., Nguyen, N., Nitchell, T., Mohabbat, K., Morgan, M., Morris, S., Nguyen, N., Nitchell, T., Mohabbat, K., Morgan, M., Morris, S., Nguyen, N., Nitchell, T., Mohabbat, K., Morgan, M., Morris, S., Nguyen, N., Nguye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 3, 2002 this sequence version replaced g1:20335511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (11-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 155023)
                                        NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "vorking draft" sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gabls1,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
                                                                                                                                                                                                                                                                                                  Sequencing vector: M13;

Chemistry: Dye-primer Bodipy: 5% of reads
Chemistry: Dye-terminator Blg Dye: 95% of reads
Chemistry: Dye-terminator Blg Dye: 95% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 141522 bases at least Q40

Consensus quality: 147097 bases at least Q30

Consensus quality: 150442 bases at least Q30

Setimated insert size: 150706; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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                                                                                                AAGTGAAGGCAAGAGGCCTCTTATTGCCCTGTGTCACCCATTTCTCCCCTTGGGTTGGCAG 55761
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36207 c 35987 g
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/db_xref="taxon:9606"
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51204: gap of unknown length
68306: contig of 17102 bp in length
68406: gap of unknown length
109481: contig of 41075 bp in length
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REFERENCE AUTHORS TITLE

JOURNAL

Direct Submission Worley, K.C.

COMMENT

Summary Statistics

3033: contig of 3033 bp in length

Center: Baylor College of Medicine Center code: BCM

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

Worley, K.C. Unpublished 2 (bases 1 Direct Submission

(bases 1 to 155023)

JOURNAL

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SOURCE
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              Clevel, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, R., David, R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Garcell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Joilvet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Li, J., Li, X., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J., Lazid, C., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J., Lazid, C., Mantiney, E., Martin, R., Martindale, A., Martinez, E., Manesey, E., Martin, R., Martindale, A., Martinez, E., Manesey, E., Martin, R., Martindale, A., Nguyen, N., Nguyen, N., Nickerson, E., Nokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rolfey, M., Shosshtari, N., Sisson, I...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC073896 182350 bp DNA linear HTG 24-. HOMO sapiens chromosome 12 clone RP11-977G19, WORKING DRAFT
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REFERENCE
AUTHORS
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BASE COUNT
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TITLE
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JOURNAL
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                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 23, 2002 this sequence version replaced of 22224602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the places

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 182350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrol, B., Thomas, N., Thomas, S. Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wieczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
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----- Summary Statistics
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Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
Project Information
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                                                                                                                                                                                               Location,
                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                  clone-"RP11-977G19"
                                                                            'chromosome="12"
                                                                                                                                                                                                                    aby4: contig of 68543 bp in 85994: gap of unknown length 182350: contig of acer.
                                                                                                                                                                                                                                                                                                2893: contig of 2893 bp in length 2993: gap of unknown length 6686: contig of 3693 bp in length 6786: gap of unknown length 17251: contig of 10465 bp in length 17351: gap of unknown length 17351: gap of unknown length
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Alignment Scores:

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Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chen, R., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorreell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 184762)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucler,A., Lucler,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mavhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Nickerson,E., Newtson,N., Nguyen,A., Nguyen,N.,
Oragunye,N., Ovledo,R., Parton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
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Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Williams,G., Williamson,A., Waeren,R., Washington,C., Walliams,G., Williamson,A., Wilczyk,R., Wooden,S., Warden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 4, 2002 this sequence version replaced g1:22094227.
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Baylor Plaza, Houston,
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as
                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid;
Sequencing vector: M13;
Sequencing vector: M13;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 183845 bases at least Q40
Consensus quality: 184849 bases at least Q20
Consensus quality: 185447 bases at least Q20
Estimated insert size: 159026; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

2040: contig of 2040 bp in length 2140: gap of unknown length

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ValProTyrAlaArgSerGluAlaH1sLeuThrGluLeuLeuGluGluIleCysAspArg
                                                                                                MetLysGluTyrGlyGluGlnIleAspProSerThrH1sArgLysAsnTyrValArgVal 108
                                                                              Submitted (26-JAN-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor. Ny 11724, USA
On Jan 26, 2002 this sequence version replaced gi:18201765.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-FEB-2001) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kirchoff,K., Kuit,K., Nascimento,L., Zutavern,T., Balija,V., Bell,M., Baker,J., Santos,L., Miller,B., Katzenberger,F., Miller,S., King,L., Yang,C., Palmer,L., O'Shaughnessy,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 207424)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="We believe the assembly to be correct. The is a mononucleotide (T) repeat in which the exact of Ts is unknown. Other subclones in the region fewer T than that represented in the assembly."

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Chen, G., Chen, R., Chen, Z., Chowdhry, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K., C., Escotto, M., Earnhart, C., Escotto, M., Elagy, N., Ford, J., Escotto, M., Frantz, P., Frantz, P., Eagn, M., Garcia, A., Halloway, C., Hamilton, K., Gorrell, J.H., Gacara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, C., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., J., Li, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucler, R., Lucler, R., Luna, R., Ma, J., Manes, E., Mashiney, E., McLeod, M.P., Meador, M., Martinez, E., Miner, S., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 12, 2002 this sequence version replaced g1:18860222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence of the pieces

* consists of 47 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
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RESULT 13 AF186113 AF	Qy 150 uPhePheSerArgGluAlaAspAsnValLysAspLysLeuCysSerLysArgThr	Qy 136Ala-CysGluSerIleValGluGluTyrGluAspGluLeuIleGl	Db 97992 AAACCAGGGAGAGAGCTGAGCCGGTGTCTCTGCCCCGGCTGAGGATCCTGGGTCACTTCT	Qy 135	Db 97932 TCTAGGCCAGCTGGAGCGATATCATAAAACCCTGTCTATAAAATCCCCCACTGCCACCCAA	Qy 135	Db 97872 CTTGTAACCCGGGCAGTGGAGGAGCAGTGGTTGGAAGATTGGCACTAGTTCATACTGAGT	.: Оу 135	Db 97812 GGAGTTCATAGGGATTCCTGGGCACAGATTGGGAGTCGGCGGGGGATATGGTGTTGCATG	Qy 135	Db 97752 ATCAGTGGCACCCTCAAGTTTGCGGTGAGTTATGGCTGTGCGGTGAGTAGCTGGTTCTTG		Qy 109 ValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp	Qy 89 MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrYalArgVal	Qy 69 ValProTyrAlaargSerGluAlaHiSLeuThrGluLeuLeuGluGluIleCysAspArg 	US-10-082-502-17 (1-182) x AC109891 (1-101666)	Alignment Scores: 2.64e-32 Length: 101 Pred. No.: 2.64e-32 Length: 99 Score: 435.00 Matches: 99 Percent Similarity: 49.75% Conservative: 0 Best Local Similarity: 49.75% Mismatches: 1 Query Match: 2 Gaps: 1	/clone="CH230-319E6" BASE COUNT 24650 a 22934 c 23569 g 23059 t 7454 o ORIGIN	4147 bp in egicus"	97420 97519: gap of unknown lend
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                                                                                                                                                                                                                                                                                          AspGlySerGlnSerValValGluVal 69
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 824)
 Submitted (17-NOV-2000) National Institutes
                       Strausberg, R.
                                                                  Homo sapiens
                                                                                              BC001027.1
                                                                                                               Homo sapiens, t
IMAGE:3344788,
                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-SEP-1999) Biomolecular Informatics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheppard, P., Jelinek, L.,
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              Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ZSIG9"
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    GATGGCAGCCAGTCAGTGGTGGAGGTA
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US-10-082-502-17 (1-182) x BC001027
                        61 AspGlySerGlnSerValValGluVal
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                                                                                                                                                                         ArgargSerGlnaspLeuHisCysGlyalaCysargalaLeuYalaspGluLeuGluTrp 40
                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: p Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6014631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., HO,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
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Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                               Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced gi:17974643.
                                                                                                                                                                                                                                                                                                                                                            Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 69753)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., I
Barbaria,J., Benton,J., Bimage, Blankenburg,K., Bor
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                                                               Center: Baylor College of Medicine
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site:
http://www.hgsc.bcm.tmc.edu/
                                                                                                        Genome Center
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REFERENCE AUTHORS TITLE

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 42 contigs. The true order of the pleces
is not known and their order in this sequence record is
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 15506 bases at least Q40
Consensus quality: 17125 bases at least Q30
Consensus quality: 18271 bases at least Q30
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49161: gap of unknown length
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51159: contig of 1898 bp in length
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54641: contig of 1908 bp in length
54741: gap of unknown length
57490: contig of 1474 bp in length
57903: contig of 1755 bp in length
59103: gap of unknown length
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60621: contig of 1518 bp in length
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                                                                                                                                          RESULT 1
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177.4
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126.4
126.8
87.2
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56.2
52.2
51.6
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49
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1017) Sheppard, P., Jellnek, L., Whitmore, T., Blumberg, H., Lehner, J. and O'Hara, P.
                                                               Mus musculus
                                                                                                 AF186115
AF186115.1 GI:6014635
                                                                           Mus musculus.
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                                                                                                                              1017 bp mRNA linear ROD 13-JAN-2000 putative secreted protein ZSIG9 (Zsig9) mRNA, complete
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AF186113
AX440375
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AC023596
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AC103156
AK094445
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AX096688
AX333297
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AX333297
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AX464040 Sequence
AX46040 Sequence
AX490465 Sequence
AB015631 Homo sapi
AC090489 Genomic s
BC001027 Homo sapi
AC109891 Rattus no
AF186113 Homo sapi
AC40375 Sequence
AC025574 Homo sapi
AC025500 Homo sapi
AC023500 Homo sapi
AC023500 Homo sapi
AC03156 Rattus no
AK094445 Homo sapi
AC033297 Sequence
AX408688 Sequence
AX408689 Sequence
AX408688 Sequence
AX408688 Sequence
AX408688 Homo sapi
AX33291 Homo sapi
AX33291 Homo sapi
AX33291 Homo sapi
AC027284 Mus muscu
AC027284 Mus muscu
AC027384 Homo sapi
AC12502 Mus muscu
AC027384 Homo sapi
AC12503 Homo sapi
AC003108 Homo sapi
AC001160 Homo sapi

BC034896 Mus muscu AK026029 Homo sapi ALL10225 Homo sapi AC033471 Homo sapi AC033473 Sequence

Database :

Pred. No.

Minimum DB Maximum DB

Title: Perfect score:

Run on: OM nucleic

Scoring table: Sequence:

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BASE COUNT
ORIGIN
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JOURNAL
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Best Local Similarity
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                  GTGGAGGTACCTTATGCCCGCTCAGAGGCCCACCTCACAGAGTTGCTTGAGGAGGTGTGT 615
                                                                                                 CACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGAAATTGCCCGCGTGGAC
                                                                                                                                                                                                                                                                                                                 CGGCCGTGGGAGCAGAGGTGGAGCGACCCTGTTACACTAAAGATGAAAGGCTGGGGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGGGCTTAGGGTCAGTTTCGGTGGGGGGCTCGCACGGGACCCTCAGATCTCCGCTTAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGAGGTACCTTATGCCCGCTCAGAGGCCCACCTCACAGAGTTGCTTGAGGAGGTGTGT
                                                                                                                                                                                                                                                          CTAGCCCTACTTTTGGGGGTECTGCTGGGAACTGCCTGGGCTCGAAGGAGCCAAGATCTA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGAAATTGCCCGCGTGGAC
                                                                                                                                                                                                                                      CTAGCCCTACTTTTGGGGGTCCTGCTGGGAACTGCCTGGGCTCGAAGGAGCCAAGATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGTCCTCGCTCGCAGGCGCTCCTAAAGCTGCCTGCTCGCGCGAGAGTTTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (14-SEP-1999) Biomolecular Informatics, ZymoGenetics,
Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sheppard, P., Jelinek, L., O'Hara, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus putative 
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative secreted protein ZSIG9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1017
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/db_xref="dbEST:AA049839"
/db_xref="taxon:10090"
/clone="IMAGE:476061"
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Homo sapiens chromosome 12 clone
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Primates;
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GACCGAATGAAGGAGTACGGGGAACAGATTGACCCTTCTACCCCACCGCAAGAACTACGTA
CGCGTCGTGAGCCGGAATGGAGAATCCAGTGAACTAGACTTACAGGGCATCCGAATTGAC 735
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                                                                                                                                                                                                                         CGGACAGATCTATGTGACCATGCCCTGCACAGATCTCACGATGAGCTATGAATCACTGGA 915
                                                                                                                                                                                                                                                                                                GAGCTTATCGAATTCTTCTCCAGAGAGGCTGACAACGTTAAAGACAAACTTTGCAGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                TCAGATATCAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAAGAATACGAGGAT
                                                                                                                                                                                                                                                                                             840
                                                                                                                                                                                                                                                                                                                                             855
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HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. DNA linear HTG 17-JUL-2001 RP11-764L14, WORKING DRAFT

Manualla; Eutheria; Frimates; Catarrhini; Hominidae; Homo.

Kanmalla; Eutheria; Frimates; Catarrhini; Hominidae; Homo.

RS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

RS Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,

Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,

Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,

Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,

Coyle,M.D., Dathorne,S.R., David,R., David,R., Delgado,O.,

Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,

Duyan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,

Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,

Foster,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,

Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,

Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,

Hernandez,J., Howard,S., Huber,J., Hollyk,S., Hane,J.,

Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,

Joudah,S., Karlsson,E., Kelly,S., Khan,U., Kanya,L., Levis,L.C.,

Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,

Loulseged,H., Lozado,R.J., Lu, Lucleer,R., Luna,R.,

Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,

Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metcker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K. Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oraguny,N., Oviedo,R., Pace,A., Payton,B., Peerry,J., Peters,L., Pickens,R., Primus,E., Pull,L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N. Mohabbat, K.,

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BASE COUNT
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Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, R., Tanerisa, R., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-OCT-1999) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2001 this sequence version replaced 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 100% of re
Chemistry: Dye-terminator Big Dye: 100% of re
Assembly program: Phrap; version 0.990329
Consensus quality: 161278 bases at least 030
Consensus quality: 174843 bases at least 030
Consensus quality: 174843 bases at least 020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: HMKZ
Center clone name: RP11-764L14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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                                                                                                                                                                                                                                                                                                                                                                                      108229: contig of 108229 bp in length 108329: gap of unknown length 150246: contig of 41917 bp in length 150346: gap of unknown length 153410: contig of 3064 bp in length 153510: gap of unknown length 15739: contig of 2229 bp in length 158199: contig of 2359 bp in length 158199: contig of 2359 bp in length
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Pred. No. 2.4e-204;
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                                                            JOURNAL
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IMAGE:2650612, mRNA, comp 
BC008261 BC008261.1 GI:14198400 MGC.
                           Direct Submission
Submitted (22-MAY-2001) National
Gene Collection (MCC), Cancer Ger
Institute, 31 Center Drive, Room
                                                                                      Strausberg, R.
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                 Mus musculus
                                                                                                                                                                 house mouse.
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Project URL:
                                                                                                                                                                                                                         transmembrane protein, mRNA, complete cds.
http://mgc.nci.nih.gov
                          National Institutes of Health, Mammalian
Cancer Genomics Office, National Cancer
ive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                        798 bp
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                 GAGGAGGTGTGTGACCGAATGAAGGAGTACGGGGAACAGATTGACCCTTCTACCCACCGC
                                        AGCCAGTCAGTTGTGGAGGTACCTTATGCCCGCTCAGAGGCCCACCTCACAGAGTTGCTT
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                                                                                                                                                                    AGCCAAGATCTACACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGAAATT 483
                                                                                                                                                         AGCCAAGATCTACACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: b Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 9903606
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar H
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/translation="KKGWGWLALLLGYLLGTAWARRSQDLHCGACRALYDELEWEIAR
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KNYVRYVSRWCESSELDLGGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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/db_xref="GI:14198401"
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NSAP is a novel saposin-like p
stimulates neurite outgrowth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-APR-2001) Neuroscience, Husargatan 3, Uppsala 75123, Sweden
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                                                                                                                /product="saposin-like protein"
/protein_id="AAK38148.1"
/db_xref="GI:20196199"
/ta_nslation="MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQ
/DPKKTIQMGSFRINPDGSQSVVEVPYARSEAHLTELLEEICDRMKEYGEQIDPSTHR
KNYVRVYGRNGESSELDLQGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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GGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCAGATGGCAGCCA
                                                                                   GGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCCA
                                                                                                                      AGATCTACACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGGAAATTGCCCG
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Sequence 17:
AX464040
AX464040.1
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Mammalia; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 0140466-A 173 Genentech Inc. (US)
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/db_xref="taxon:9606"
316 c 379 g 25
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Eutheria; Primates; Catarrhini; Hominidae;
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0; Mismatches
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No. 2e-176;
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                   GGTCCTGCTGGGAACTGCCTGGGCTCGAAGGAGCCAAGATCTACACTGTGGAGCTTGCAG
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GGCTCTGGTGGATGAATTAGAGTGGGAAATTGCCCCGCGTGGACCCCAAGAAGACCATTCA
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                                                                                                                                           AGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTG-TAGTTTCGGGAGCCACTGGGGCCC
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Sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                       CORIXA
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Lodes,M.J., Algate,P.A., Fling,S.P.,
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/db_xref="taxon:9606"
194 c 241 g 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGAATCCAGTGAACTAGACTTACAGGGCATCCGAATTGACTCAGATATCAGCGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JUN-1998) Seishi Kato, Research Institute Rehabilitation Center for the Disabled, Department of Rehabilitation Engineering; 4-1 Namiki, Tokorozawa, Sait 359-8555, Japan (E-mail:seishi@rehab.go.jp, Tel:042-995-3100(ex.2568), Fax:042-995-3132)
                                                                                                                                                      Selection of CDNAs encoding putative type II membrane the cell surface from a human full-length cDNA bank Gene 228 (1-2), 161-167 (1999)
                                                                                                                                                                                                                                              AB015631

AB015631.1 GI:4586839

type II membrane protein.

Homo sapiens gastric adenocarcinoma clone_lib:pKA1-meta-1 clone:HP10390.

Homo sapiens
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                                                                                                                        Direct Submission
                                                                                                                                  Kato, S.
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                  Homo sapiens mRNA clone: HP10390.
                                                                                                                                                                                                                                                                                                                                     AB015631
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HP10390"
/tissue_type="gastric add
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CDS

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/codon_start=1

BASE COUNT ORIGIN

210

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Query Match Matches 701;

Conservative

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Score 606.6; DB 9; Pred. No. 1.5e-153; 0; Mismatches 94;

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213 AGAAGCCGGGACAGCCCCGTTTTTCCCCAGCCAGCTGCTAGGGTTGGGACCCCACAGAAAAC
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                                                                                                         AACGTGATGGAACACCCCCAGGAGGGGAAGATGGCCAGTTGCCTTT--TATATTACGTT
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Best Local Similarity
Matches 321; Conserv
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GTGCCTAGTTAAGTGCGGGAAGCTGGGCCAGGCGGTCACTGGCCACCCTGAACCTGGCGG
                                                   GTGCCTAGTTAAGTGCGGGAAGCTGGGCCAGGCGGTCACTGGCCACCCTGAACCTGGCGG 195
                                                                                                                           GGCGGGCTTAGGGTCAGTTTCGGTGGGGGGGCTCGCACGGGACCCTCAGATCTCCGGCTTAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-JAN-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor. Ny 11724, USA
On Jan 26, 2002 this sequence version replaced gi:18201765.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one Mill subclone; and the assembly was confirmed by restriction digest.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCombie, W.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-FEB-2001) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic sequence for Mus musculus, clone RP23-104010, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McCombie,W.R., de la Bastide,M., Spiegel,L., Preston,R.,
Kirchoff,K., Kuit,K., Nascimento,L., Zutavern,T., Balija,V.,
Bell,M., Baker,J., Santos,L., Miller,B., Katzenberger,F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muller,S., King,L., Yang,C., Palmer,L., O'Shaughnessy,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 207424)
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-104010"
/clone_11b="RPCI-23"
48132.48165
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/Mote="We beleve the assembly to be correct. The sequency for the sequency of Ts is unknown. Other subclones in the region show one fewer T than that represented in the assembly."

4 48671 c 49663 g 56477 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                               clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: p Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6014631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Berokstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Karlins,E., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Thongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 824)
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IMAGE:3344788,
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/translation="mkGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQ VDPKKTIQMGSERINPDGSQSVVEVTVTVPPNKVAHSGEG" 194 c 233 g 176 t
                                                                        /codon_start=1
/product="transmembrane |
/protein_id="AAH01027.1"
/db_xref="GI:12654403"
                                                                                                                                                                                                                              /tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="LocusID:10330"
/db_xref="taxon:9606"
                                                                                                                                                                                                    /note="Vector:
                                                                                                                                                                                                                                                                                                      /clone="MGC:1545 IMAGE:3344788"
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ne MGC:1545
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                                                      GGAGCCAAGATCTACACTGTGGAGGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGAAA 481
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KEYWORDS LOCUS RESULT 10 AC109891 SOURCE , ACCESSION REFERENCE AUTHORS ORGANISM Barbaria, J., Benton, J., Bindege, K., Blankenburg, K., Bonnin, D., Binderburg, K., Brown, M., Bryant, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulkey, C., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guezara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hubey, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C. Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., AC109891.3 GI:21738196 HTG; HTGS_PHASE1. Rattus Eukaryota; Metazoa; Mammalia; Eutheria; AC109891 ***, 47 unordered pleces AC109891 Rattus. Norway (bases 1 to 101666) norvegicus rat pieces. Chordata; Rodentia; 101666 bp DI ne CH230-319E6, Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; DNA * * * linear SEQUENCING IN PROGRESS Allen, C., 13-JUL-2002

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Direct Submission
Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 101666)
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On Jul 12, 2002 this sequence version replaced g1:18860222.
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Direct Submission
                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 47 contides. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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2 (bases 1
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Center clone name: GOKY
Center clone name: Clar30-319E6
Sequencing vector: plasmid
Chemistry: Dye-terminator Big Dye:
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Consensus quality: 60229 bases at least 040
Consensus quality: 63559 bases at least 030
Consensus quality: 66730 bases at least 020
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Contact: hgsc-help@bcm.tmc.edu
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Web site: http://www.hgsc.bcm.tmc.c
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AF186113.1
                                                     Submitted (14-SEP-1999) Biomolecular Informatics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102,
                                                                          Direct Submission
                                                                                               Sheppard, P., Jelinek, L.,
                                                                                                                    Homo sapiens putative 
Unpublished
                                                                                                                                                    Sheppard, P., Jelinek, L.,
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                          Homo sapiens putative secreted
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 /organism="Homo sapiens"
/db_xref="dbEST:R15306"
/db_xref="taxon:9606"
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1..10166
/organism="Rattus norvegicus"
/ob_xref="taxon:10116"
/clone="CH230-319E6"
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                                                                                                                                                                                                                                                                                                                                                 GGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCCAGGTGGACCCCAAGAAGACCATTC
                                                                                                    Patent: WO 0190154-A
                                                                                                                         Compositions and methods
                                                                                                                                        Xu,J., Mitcham,J.L., Harlocker,S.L.,
Lodes,M.J., Algate,P.A., Fling,S.P.,
                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
142 c 152 g 11
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="12"
/map="12q15"
/clone="IMAGE:29675"
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Thomas, S., Tang, H.,

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                                Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonkin, D., Bouck, J., Bowle, S., Bileva, M., Brown, E., Brown, M., Bryant, N. P., Bouck, J., Bowle, S., Bileva, M., Brown, E., Brown, M., Bryant, N. P., Bouck, J., Bowle, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, R., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Chen, R., Chen, R., Chen, R., L., Dadthorne, S. R., David, R., J., Franguto, D., Edward, C. C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edward, C., C., Lihaj, C., Escotto, M., Gorrell, J. H., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Gao, J., Hale, S., Hamilton, K., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Huber, J., Hale, S., Hume, J., Jackson, L. E., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Liu, W., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Liu, W., Loulseged, H., Mansey, E., McLed, R., Martindale, A., Martinez, E., McLed, R., Martindale, A., Martinez, E., McLed, R., Martindale, A., Martinez, E., McLed, R., Payton, B., Perez, L., Perez, L., Polles, R., Polloban, I., Rojuen, M., Rojuen, N., Rojuen, N., Rojuen, N., Rojuen, N., Rojuen, N., Rojuen, N., Rojuen, R., Stanley, H., Sto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens SEQUENCE, 12 AC025574
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1 (bases 1 to 155023)
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HTG; HTGS_PHASE1; HTGS_D
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                        Sparks, A., Stanley, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 12 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission

Direct Submission

Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 3, 2002 this sequence version replaced g1:20335511.
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Submitted (11-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 155023)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S. Usmani, K., Vasquez, L., Veza, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wieczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley, K.C
Direct Sub
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Sequencing vector; M13;
Chemistry: Dye-primer Bodipy: 5% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 141522 bases at least 040
Consensus quality: 147097 bases at least 020
Consensus quality: 147097 bases at least 020
Estimated insert size: 150706; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project information
Center project name: HALV
Center clone name: RP11-348M3
                                                                                                                      31879
42264
42364
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Contact: hgsc-help@bcm.tmc.edu
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5972
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    109481:
109581:
                                                                                                                                                                                                                                                                                             3: contig of 3033 bp in le

3: gap of unknown length

contig of 2838 bp in le

: gap of unknown length

: contig of 4198 bp in le

: gap of unknown length

: contig of 2640 bp in le

: gap of unknown length

: contig of 4464 bp in le
                   gap of contig gap of contig
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Of
                                                                              f unknown length
g of 8741 bp in la
f unknown length
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g of 7028
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              unknown length of 41075 bp in
                                                             unknown leng
of 17102 bp
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        Allen, C., Adians, C., Adians, C., Adians, E., Allen, C., Are, J.R., Ayele, M., Banks, T., Barbbria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bovie, S., Birleva, M., Brown, E., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, Z., Chowdhy, I., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, R., Fortaguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Edwards, C.C., Elhaj, C., Escotto, M., Earlbay, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, N., Ferraguto, D., Flagy, N., Hale, S., Hahels, S., Hamilton, K., Sarrier, P., Hale, S., Hamilton, K., Sarrier, T., Garza, N., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Jackson, E., Kallsson, E., Kallsson, E., Kallsson, E., Kallsson, E., Kollins, B., Lewis, L.C., Lewis, L., Lichtarge, O., Lieu, J., Liu, J., Liu, R., Ma, J., Lozado, R., Lucier, R., Lucler, R., Lund, R., Ma, J., Lozado, R., Martinez, E., Massey, E., Machiney, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Martinez, 
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AC073896
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/db_xref-"taxon:9606"
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Pred. No. 1.3e-36;
0; Mismatches 21
  Pace, A., Payton, B.,
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clone RP11-977G19, WORKING DRAFT
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Peters, I., Pickens, R., Primus, E., Pu, I.I., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rulf, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshtari, M., Rulf, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshtari, M., Sison, I., Stone, H., Shoshtari, M., Sison, I., Stone, H., Shoshtari, M., Stone, H., Shoshtari, M., Stone, H., Shoshtari, M., Stone, H., Shore, H., S
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* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

2893: contig of 2893 bp in length

2994

6686: gap of unknown length

6687

6786: gap of unknown length

17252

17251: contig of 16045 bp in length

* 17252

17351: gap of unknown length

* 17252

17351: gap of unknown length

* 183895

85994: gap of unknown length

* 183895

85994: gap of unknown length

* 10.182350

Coration/Qualifiers

ce

/organism="Homo sapiens"

/chromosome="12"

/clone="RP11-97G19"

46453 a 45416 c 43855 g 46174 t 452 others
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REFERENCE
AUTHORS
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KEYWORDS
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Best Local Similarity 90.0%;
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ARBITONS, S. L., Amazatunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarla, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox.C., Coyle, M.D., Dathorne, S. R., David, R., Delanoy, K.R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H.H., Bearnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, D. A., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisia, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudsh, S., Kratovic, J., Kureshi, A., Landry, N., Leel, B., Lewis, L., C., Lewis, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Massey, E., Mawhiney, E., McLeod, M.P., Maedor, M., Mel, G., Metzker, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Martin, R., Martindale, A., Martinez, E., Mayne, N., Nickerson, E., Put. L., Norgan, A., Nguyen, N., Scherer, S., Scott, G., Shen, H., Shoshhari, N., Sisson, I., Sutton, A., Syatek, A., Francy, F., Sparks, A., Francy, G., Sodergyen, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, N., Thomas, N., Thomas, N., Thomas, S., Warren, R., Warren, R., Warren, R., Marting, C., Watlington, S., Wang, G., Warren, R., Warren, R., Wang, G., Marting, R., Wang, G., Marting, R., Wang, G., Marting, R., Wang, G., Warren, R., Warren, R., Stanley, H., Stone, H., Ston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 675 ACGCGTCGTGAGCCGGAATGGAGAATCCAGTGAACTAGACTTACAGGGCATCCGAATTGA 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 184762)
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Homo sapiens chromosome 12 clone RP11-183H16, WORKING DRAFT
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Pred. No. 1.3e-36;
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                                                                                                                                          source
     47425
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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 9 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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On Aug 4, 2002 this sequence version replaced g1:22094227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-FEB-2000) Human Genome Sequencing Center, Department of MoLecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid;
Sequencing vector: plasmid;
Sequencing vector: min;
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: phrap; version 0.990329
Consensus quality: 183845 bases at least 030
Consensus quality: 184849 bases at least 030
Consensus quality: 18447 bases at least 030
Consensus quality: 185447 bases at 
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Center project name: HAFC
Center clone name: RP11-183H16
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Contact: hgsc-help@bcm.tmc.edu
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Zhou,J., Zorrilla,S., Nelson,D.,
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clone="RP11-183H16" 44751 c 45101 c

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Human Zs1g9 gene e Human secreted pro Human secreted exp Mouse secreted exp cDNA sequence #398

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Minimum DB
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2011.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secretory peptide-9; Zsig9; orthologue; mouse; tumour marker; cancer; therapy; diagnosis; growth enhancer; ss.
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                                                                                                  02-JUL-1998;
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                                                                                                                                                                                                                                                                       mat_peptide
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Human pancreatic c Human genomic DNA Human polynucleoti Human secreted pro Gene #135 used to Lung cancer relate

Mouse spliced tran Gene #1334 used to Lung cancer relate Human spliced tran

Human prostate exp Human prostate exp

Human ovarian tumo
Human breast cance
Human breast cance
Human secreted pro
Human secreted pro
Human pancreatic c
Human genomic DNA

Human secreted pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA clone encodes novel mouse secretory peptide-9, or 2sig9
( (see AAW88476), an orthologue of novel human 2sig9 (see AAW88469).

CHUMAN Zsig9 is overexpressed in a number of tumours including brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors, and thus can be used as an indicator for cancer. The invention provides polynucleotides (see AAW88469-70) including mature polypeptides, other processed forms, variants and the mouse orthologues. The Zsig9 gene, or probes derived from it, can be used to determine if zsig9 is present on chromosome 10, and if a mutation has occurred. Antibodies raised against 2sig9 can be used as diagnostic agents to determine the presence of zsig9, and thus the presence of cancer. They can also be labelled with radioisotopes or fused with toxins and used to treat tumours which overexpress 2sig9. Antisense nucleotides derived from Zsig9 colarents, heart or liver
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Matches 1069; Conserv
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cDNA can also be used to innimize cDNA can also be used to enhance the proteins can be used to enhance the nlacenta, heart or liver.
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Mature_Zsig9_protein_variant-4
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Query match
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CDNA; 1210 ВP

entry)

sequence encoding for PRO4426 polypeptide.

breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeietal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss. secretory and transmembrane; PRO; mammalian; cancer; lung;

99WO-US28301

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                                                                                                                                                                                                                                                                                                                                                                   PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC come of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC control teration or differentiation of chondrocytes, the proliferation or cc control teration of inner ear utricular supporting cells or CC cartilage, the proliferation of inner ear utricular supporting cells or T-lymphocytes, the release of a cytokine from peripheral blood cc monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides and modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide consecutes involved in binding interactions. The polypuclectides encoding CC molecules involved in binding interactions. The polypuclectides encoding CC to factor vira. The PRO polypeptides can be used in gene therapy.
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Matches 850; Conserv
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                                                                                                                                                                                                                                                                                                                                              Sequence
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2000WO-USO5004.

2000WO-USO5001.

2000WO-USO5601.

2000WO-USO7377.

2000WO-USO7337.

2000WO-USO8439.

2000WO-US13705.

2000WO-US14042.

2000WO-US15264.

2000WO-US15264.
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"attanabe CK, Wood WI,
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                                                                                                                 Human; secreted protein; gene therapy; protein therapy; tissue; cance tumour; neurodegenerative disorder; leukaenia; autoimmune disease; AI developmental abnormality; discase; leukaenia; lathelimer's disease; cognitive disorder; schizophrenia; immunological disorder; mood disor immune deficiency disease; respiratory disorder; arthritis; skeletal; haematopoietic disorder; neural; osteoporosis; metabolic disorders;
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용
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CC encoding human secreted proteins (AAY01135) to AAXV01159). The secreted
CC protein gene sequences are deposited with the ATCC under deposit number
CC ATCC 209118. Host cells comprising recombinant vectors containing the
CC nucleic acid sequences are used for the recombinant production of the
CC secreted proteins. The polynucleotide and amino acid sequences are useful
CC for are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Pathological conditions can
CC be also diagnosed by determining the amount of the new polypeptides in a
CC sample or by determining the presence of mutations in the new
CC polynucleotides. Specific uses are described for each of the
CC cancer, tumours, developmental abnormalities and social deficiencies,
CC cancer, tumours, developmental abnormalities and cognitive disorders,
CC schizophrenia, immunological disorders, immune deficiency diseases
CC (AIDS), mood disorders, neural disorders, arthritis, asthma,
CC osteoporosis, metabolic disorders, caralovascular disorders, sendocrine
CC disorders or gastrointestinal disorders. The polypeptides are also useful
CC for identifying their binding partners. The present sequence represents a
CC combine and clone identification (see descriptor line for gene
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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01-JUL-1997;
01-JUL-1997;
12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, immune deficiency diseases or blood
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1180 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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DB; AAY01136, AAY01162,
                                                                                                                                    GCTTAGGTGCCTAGTTAAGTGCGGGAAGCTGGGCCAGGCGGTCACTGGACCCTGAACC
                                                                                                                                                                                                    GAGGGGCGGCTTAGGGTCAGTTTCGGTGGGGGGCTCGCACGG--GACCCTCAGATCTCC
                           TAGGGTTGGGACCCACAGAAAACAAAGTGAGAGTCCGGCTGCTTTCCAGAGCCTGGGCCA
                                                                        GAGGGGCGGGTTTGGGGTCTGGTGTTGGGGGCTCGCACCGCAGCACGCTGGAGTCCC
                                                                                                                                                                                                                                               GACCGGGGTCCTTGCTGTTCGGGAGCCTCTCCT-AAGCTGCCTGTTCGCGCGARAKTTTG
                                                        TGTGGCAGGCGGAAGCTCTGGAGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTG-
                                                                                                                      GCTTAGGTACCAGTTAGCGTCAGGGGAGCTGGGTCAGGCGGTCGCCGG-GACACCCCGTG
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                     Identifying modulators of a cancer-related gene to screen agents preventing or treating cancer comprises detecting a difference in expression of cancer-linked genes in the presence or absence of compounds
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DB; AAU97063.
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                                                                                                                                                                                                                                                                                                                                                                                  sequence tag; EST; h
T lymphocyte; chemot!
rane protein 4; gene;
                                                                                                 Horrigan
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2000US-239297P.

2000US-239602P.

2000US-239802P.

2000US-239806P.

2000US-240622P.

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                                                                                                                                                                                                                                                                                                                                                                                           EST; human; cancer; anti-neoplastic; chemotherapy; cytostatic; chromosome
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Best Local S
Matches 701
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                                                                                                          CCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTT
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                                                                                                                                        The specification describes a method of antibody preparation. The method comprises inoculating an animal with a vector expressing a fusion protein having an antigen protein fused to the C-terminal side (extracellular) of a transmembrane domain protein (the N-terminal side of which is intracellular), and then isolating and purifying the antibody from the animal. The antibodies can be used as drugs, vaccines, diagnostic reagents and laboratory reagents. The present sequence encodes a polypeptide, designated HP10390, which we used in the course of the invention.
                                                                                                                                                                                                                                                                                    Antibody preparation by inoculation of an animal with a vector expressing a fusion protein of an antigen on the C-terminal side transmembrane domain for use as drugs, diagnostic reagents and
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                                                                                                                      Sequence
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24-AUG-2000; 2000JP-0254407
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DB; ABB09717.
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24-MAY-2000;
                                        WO200190154-A2
                                                                                       Human ovarian
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                                                      Homo sapiens
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                                                                  n; ovarian tumour protein; cancer; cytostatic; immunostimulant; therapy; CD4+ T cell; CD8+ T cell; PCR primer.
                                                                                                                                                                                                    AACGTGATGGAACACCCCCAGGAGGGGAAGATGGCATTGCCTTT--TATATTACGTT
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2000US-207107P
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              2001WO-US16895
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21-JUN-2000; 2000US-213673P.
03-AUG-2000; 2000US-223288P.
01-MAR-2001; 2001US-272790P.
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                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                 2002-097641/13.
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PA, Fling SP,
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P, Mannion J,
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Benson
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New isolated polynucleotide encoding polypeptide comprising ovarian tumour protein, useful for detection, diagnosis and human ovarian cancer portion င္က င္က

Claim 1; Page 253-254; 285pp; English

The invention relates to an isolated polynucleotide encoding a polypeptide comprising a portion of an ovarian tumour protein. The sequences of the invention are useful for stimulating an immune response and for treating ovarian cancer in a patient. An antigen presenting cell that expresses the sequences is useful for treating ovarian cancer by incubating CD4+ and/or CD8+ T cells isolated from a patient. The T cells can then be proliferated and administered to the patient to inhibit the CC can then be proliferated and administered to the patient to inhibit the CC for nucleic acid hybridisation, to direct expression of a polypeptide in appropriate host cells. Detecting the presence of a cancer in a patient converse obtaining a biological sample from the patient, contacting the biological sample with an agent that binds to the protein, detecting the amount of protein that binds to the agent, comparing the amount of protein that binds to the agent, comparing the amount of cancer. Sequences ABK09464-ABK09802 represent PCR primers and cDNA cancer can be compared to the convention.

Sequence 814 BP; 210 A; 194 C; 241 <u>ი</u> 169 T; 0 other;

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Query Match
Best Local S
Matches 701
 701;
          Similarity
  Conservative
          56.7%;
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         Score 606.6; DB 24; Length 814; Pred. No. 1.2e-147;
  Mismatches
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Gaps
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180 GGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAG 239	393 GGTCCTGCTGGGAACTGCCTGGGCTCGAAGGAGCCAAGATCTACACTGTGGAGCTTGCAG 452
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N	240 GGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCATTCA 2	240
u	453 GGCTCTGGTGGATGAATTAGAGTGGGAAATTGCCCGCGTGGACCCCAAGAAGACCATTCA 5:	453
N	180 GUCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAG 2	Tac

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41	b 360 CCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTA 419	밁
σ	y 573 CCGCTCAGAGGCCCACCTCACAGAGTTGCTTGAGGAGGTGTGTGACCGAATGAAGGAGTA 632	Ş
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03-JUL-1997;
19-MAY-1998;
19-MAY-1998;
17-JUN-1998;
                                   Claim 2;
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                                                                                                                                                                                                                                    ZYMOGENETICS INC.
                         Page 73-74; 85pp; English
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growth enhancer;
                                                                              n secretory peptide-9 (Zsignate) placenta, liver and heart,
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97US-0051704.
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variant; ss.
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heart, and
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CC variant (see AAW88474). Zsig9 (see also AAW88469) is overexpressed in
CC human brain, liver, lung, oesophageal, stomach, colon, rectal,
CC thyroid and lymphoma tumors. Thus, Zsig can be used as an
CC clone from a full-term pregnancy cDNA vas discovered in a placenta
CC clone from a full-term pregnancy cDNA library which contained an
CC clone from a full-term pregnancy cDNA library which contained an
CC clone from a full-term pregnancy cDNA library which contained an
CC clone from a full-term pregnancy cDNA library which contained an
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CC clone from a full-term pregnancy cDNA library which contained an
CC clone from a full-term pregnancy cDNA library which contained an
CC clone from a full-term pregnancy cDNA can also be used to determine if Esig9 gene, or probes derived
CC variants and mouse orthologues. The Zsig9 gene, or probes derived
CC liprance from the contained and containe
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AAACGTGATGGAACACCCCCAGGAGGGGAAGATGGCAGCATTGCCTTT--TATATTACGT
                                                 TCTCCAGAGAGGCTGACAACGTTAAAGACAAACTTTGCAGTAAGCGGACAGATCTATGTG
                                                                                                                                                                                                                        CCCTCAAGTTTGCGTGTGAGAGCATTGTGGGAAGAATACGAGGATGAGCTTATCGAATTCT
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The present DNA sequence is a gene encoding the variant of the secretory protein 9, 2sig9 that arises due to alternative splicing, allelic variation or silent mutations that result in amino acid changes. This sequence is mapped to the human chromosome 12q15 region. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to 2sig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to zsig9 and it may be radio-labelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding zsig9. The Zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting
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nucleotides
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                                                                                                                                                                                  tumors using antibodies, antagonists es to secretory protein-9 (2sig9)
                                                                                                                                                                                                                                                               Taft
                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene encoding secretory protein variant-4.
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/note= "Overexpressed in tumours"
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Mature_Zsig9_protein_variant-4
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RESULT 11 AAX97837

AAX97837

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AAX97837;

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Best Local Sim
Matches 690;
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                                                                TGGCTTGATGGATCACCCCCAGGAGGGGAAAATGGTGGCAATGCCTTTTATATATTATGT
                                                                          AAACGTGATGGAACACCCCCAGGAGGGGGAAGATGGCATTGCCTTT--TATATTACGT
                                                                                                                                                                           CCCTCAAGTTTGCGTGTGAGAGCATTGTGGGAAGAATACGAGGATGAGCTTATCGAATTCT
                                                                                                                                                                                                             ATGGAGAATCCAGTGAACTAGACTTACAGGGCATCCGAATTGACTCAGATATCAGCGGCA
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87.7%;
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No. 1
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Best Local Similarity
Matches 722; Conserv
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diagnostic, forc.
also include d
                                                                                                                                                                                                                                                                                                                                                               AAX97813-x97906 represent extended cDNA's which encode novel human secreted proteins (see AAY36129-Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.
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13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
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TGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGA
                   TGCCCGCTCAGAGGCCCACCTCACAGAGTTGCTTGAGGAGGTGTGTGACCGAATGAAGGA
                                        GGGGTCCTGCTGGGAACTGCCTGGGCTCGAAGGGGCCAAGATCTACACTGTGGGGCTTGC
                                                                                                                                                                     AGGTGGAGCGACCCTGTTACACTAAAGATGAAAGGCTGGGGTTGGCTAGCCCTACTTTTG
                                                                                                                            GGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAGCATGC
                                                                                                                                                                                                                CCAAAGTGAGAGTCCAGCGGTCTTCCAGCGCTTGGGCCACGGCGGCGGCGCCCTGGGAGCAG
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97US-0066677.
97US-0069957.
98US-0074121.
98US-0081563.
98US-0096116.
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85.9%;
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09-FEB-1998;
13-APR-1998;
10-AUG-1998;
   Claim 1; Page 272; 307pp;
                  Extended
                                                Bougueleret L,
                                                                                                                                                             Homo
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               cDNAs encoding secreted proteins
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97US-0066677.
97US-0069957.
98US-0074121.
98US-0081563.
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                                                                                                                                                                        therapy;
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                                             GCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAAGAATACGAGGATGAGCTTATCG
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                                                                                           ----ACTGGCTTGATGGATCACCCCCAGGAGGGGAAAATGGTGGCAATGCCTTTTATATA
                                                                                                                                                                                        TACACCAAACGTGATGGAACACCCCCCAGGAGGGGAAGATGGCAGCAGTTGCCTTT--TATA 983
                                                                                                                                                                                                     AATTCTTCTCCCAGAGAGGCTGACAACGTTAAAGACAACCTTTGCAGTAAGCGGACAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTGGGGGTCCTGCTGGGAACTGCCTGGGCTCGAAGGGCCCAAGATCTACACTGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
639; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             714 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 A; 158 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 G; 151 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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les 73;
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AAA43525;

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329 AGAGGTGGAGCGACCCTGTTACACTAAAGATGAAAGGCTGGGGTTGGCTAG-CCCTACTT 387

Best Local Signatches 550; Query Match

Similarity

48.08; 97.78;

Score 513.4; Pred. No. 1.7e 0; Mismatches

.7e-1

ω

Gaps

Conservative

0;

Sequence 592 BP; 159

A; 139 C; 167 G; 123 T; 4 other;

AAA43525 standard; cDNA; 592

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CC AAA43426 to AAA45925 represent specifically claimed secreted expressed CC sequence tags (SESTs), isolated from human, mouse, chicken and rat CC tissue sources. The SESTs can have a range of activities depending on CC the tissues they were isolated from. The activities include: CC chemotactic; proliferative; immunomodulatory; haematopoletic; cc chemotactic; antipacterial; antifungal; antivital; antifinflammatory; CC cytostatic; antibacterial; antifungal; antivital; antifinflammatory; CC antiasthmatic; vulnerary; antilucer; osteopathic; neuroprotective; CC notropic; antiparkinsonian; antipsoriatic; cerebroprotective; CC notropic; antiparkinsonian; antipsoriatic; cerebroprotective; CC enticonvulsant; and antidepressant. The SESTs can be used for gene CC therapy and in vaccines. The SESTs are useful as probes for the CC identification and isolation of full-length cDNAs and genomic DNA CC molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising CC antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions CC (asthma), myeloid or lymphold cell deficiencies, wounds, burns, ulcers, costeoporosis, osteoparthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's CC disease), tumours, bacterial, fungal or viral infections, depression and cc in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; expressed sequence tag; sEST; probe; chemotactic; proliferative; immunomodulatory; haematopoletic; chemokinetic; analgesic; haemostatic thrombolytic; antilnflammatory; cytostatic; antibacterial; antifungal, antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiviral; osteopathic; neuroprotective; nootropic; antiparkinsonian; antilocer; osteopathic; neuroprotective; nootropic; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoparosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 228-229; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacobs K,
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                                                                                          depression and
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RESULT 14
ABK36007
ID ABK36
XX ABK36
AC ABK36
XX O8-MJ
XX O8-MJ
XX Humaa
KW Humaa
KW Infe
KW Infe
KW Unoc
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                                     Merberg D,
Clark HF,
WPI; 2002-179322/23
                                                                                                                                                                                                                                                                                                                                Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene
                                                                             Jacobs K,
                                                                                                                                                 06-APR-2000; 2000US-195605P
                                                                                                                                                                                         29-MAR-2001; 2001WO-US10232
                                                                                                                                                                                                                                     18-OCT-2001
                                                                                                                                                                                                                                                                        WO200177289-A2
                                                                                                              (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequence #398 encoding novel human secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK36007 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGACCATCCCCTGCACAGATC 575
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Treacy M, /
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                                 Lavallie ER,
Agostino MJ,
Howes SH, Re
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                         Collins-Racie LA, Evar
J, Bowman MR, Spaulding
Resnick RJ, Gulukota K,
                                               Evans
ding V,
                         V, Wong GG;
Graham JR;
                                                              ü
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Six hundred and twenty three polynucleotides derived from a variety human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders. disorders of.

Claim ŗ Page 393pp; English.

The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been controlled from a variety of human tissues. The invention also provides the proteins are useful for identifying compounds that modulate their cartity and production. The sequences of the invention are useful for identifying compounds that modulate their cartity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined condectioncy (SICD)), autoimmune disorders (e.g. multiple conditions (e.g. arthritis), infectious disorders (e.g. hepatitis), allowed disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allowed film (e.g. arthritis), neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. fivention are also useful in gene therapy. ABK35610-ABK30232 represent conditions (e.g. asterna), neurodesed for novel human care accurated proteins.

Sequence 657 BP; 177 A; 149 C; 185 G; 146 T; 0 other;

밁 Š ₽ Ş 밁 Ş 밁 Q 밁 Ş ₽ Ş 밁 Ş, В Ş ₽ Ş 밁 Ş Query Match Matches 910 481 850 421 790 361 730 241 301 670 610 181 550 121 490 430 370 GGTTGGCTAGCCCTACTTTTGGGGGTCCTGCTGGGAACTGCCTGGGCTCGAAGGAGCCAA 429 61 Local Similarity hes 571; Conserv _ ACTGGAGCAGCCCAC----ACTGGCTTGATGGATCACCCCCAGGAGGGGAAAATGGTGG ACTGGAGCAAGCAGCCTACACCAAACGTGATGGAACACCCCCCAGGAGGGGAAGATGGCAG AGTAAGCGGACAGATCTATGTGACCATGCCCTGCACAGATCTCACGATGAGCTATGAATC GAGGATGAACTCATTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGC GAGGATGAGCTTATCGAATTCTTCTCCAGAGAGGGTGAGAAACGTTAAAGACAAACTTTGC TACGTACGTGTAGTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGA TCAGTTGTGGAGGTACCTTATGCCCGCTCAGAGGCCCACCTCACAGAGTTGCTTGAGGAG TACGTACGCCGTCGTGAGCCGGAATGGAGAATCCAGTGAACTAGAGTTACAGGGCATCCGA ATATGTGACCGGATGAAGGAGTATGGGGAACAGATTGATCCTTCCACCCATCGCAAGAAC GTGTGTGACCGAATGAAGGAGTACGGGGAACAGATTGACCCTTCTACCCACCGCAAGAAC GATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCCAC GATCTACACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGAAATTGCCCGC 489 Conservative 47.18; 88.48; 0, Score 503.2; DB Pred. No. 8e-121; 0; Mismatches 6 68; 24; Indels Length 7; Gaps 969 540 909 480 849 420 789 360 729 300 669 240 180 549 609 120 ž

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CATTGCCTTT--TATATTACGTTTTTATGGAAATGAACTGAAAAAA

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RESULT 15
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ID AAZ38
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                                                                           Query Match 44.2%;
Best Local Similarity 91.6%;
Matches 500; Conservative
                                                                                                                                                              This sequence represents the coding sequence of human cDNA clone HP10390 which encodes a 20 kD protein with one putative transmembrane domain in the N-terminus. The cDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists
                                                                                                                                                                                                                                                                                                                                    (SAGA )
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HP10390; transmembrane domain; stomach cancer cell; antibody; assay reagent; diagnostic marker; primer; probe; antisense; gagonist; antagonist; ligand; therapeutic; ds.
                                                                                                                                                                                                                                                                                                            Claim 3; Page 88; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09955862-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human transmembrane protein cDNA clone HP10390 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ38326 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                   ATGAAAGGCTGGGGTTGGCTAGCCCTACTTTTGGGGGTCCTGCTGGGAACTGCCTGGGCT 417
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                         2000-023358/02.
                                                                                                                                                      are potentially useful therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAGAMI CHEM RES CENT PROTEGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                        AAY52391.
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                                                                                                                               546
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                                                                                                                              139 A; 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human transmembrane protein HP10390"
"No stop codon given in the specification"
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                                                                                                                            C; 165 G; 116 T; 0 other;
                                                                           Score 472.4; DB 21; Length 546; Pred. No. 7.5e-113; 0; Mismatches 46; Indels 0;
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                                       GACAAACTTTGCAGTAAGCGGACAGATCTATGTGACCATGCCCTGCACAGATCTCACGAT
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                  GAGCTA 903
                                                                                 GTGGAAGAATACGAGGATGAGCTTATCGAATTCTTCTCCAGAGAGGCTGACAACGTTAAA 837
                                                                                                                                                                                 CACCGCAAGAACTACGTACGCGTCGTGAGCCGGAATGGAGAATCCAGTGAACTAA
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Search completed: March 30, 2003, 18:47:39 Job time: 261.709 secs

Sequence Sequence Sequence

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Result
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Perfect score:
Sequence:
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Maximum DB
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
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US-08-232-463-14
US-09-213-810-1
US-09-202-548B-5
US-09-202-548B-5
US-09-202-56-11
US-09-202-956-11
US-09-202-956-11
US-09-2030-607-110
US-09-439-313-110
US-09-332-149A-110
US-09-332-149A-110
US-09-332-149A-110
US-09-132-060-41
US-08-122-126A-4
PCT-US95-0425B-4
US-08-311-56B-3
US-08-385-119A-1
US-08-385-982-542
US-08-888-07-78-4
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                                 Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 110, App Sequence 100, App Sequence 100, App Sequence 100, App Sequence 1, Appli Sequence 41, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1,
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US-08-738-349-1
                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/364
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:

NAME: BAIKET, M. P.

REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 0248
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs

TYPE: nucleic acid.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application Patent No. 5869638
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ORIGINAL SOURCE:
               MOLECULE TYPE:
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TITLE OF INVENTION: Bone-Related Cadherin-Like Protein
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                               STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1300 I STREET: Washington
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COUNTRY: US
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1300 I Street, N.W.
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Kawai, Shinji
Tsujimura, Atsushi
                               linear
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             cDNA to mRNA
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26-AUG-1993
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FR: 02481.1323-00000
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US-08-9721-822A-10
US-08-952-500-1
US-08-195-006-1
US-08-195-07644A-1
US-08-524-757-1
US-09-206-903A-11
US-09-206-903A-11
US-09-206-935-2
US-09-206-935-3
US-09-206-936-3
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US-08-232-463-14/c
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Best Local Similarity 63.6%;
Matches 70; Conservative
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                Best Local Similarity
                            Query Match
  Matches
                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPERICATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
STRAIN: O
FEATURE:
                                                                   IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                     TOPOLOGY:
                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                nucleic acid
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                                                                                                                                            7218 base pairs
                                                                                                                                                                                                       : (703)836-9300
(703)683-4109
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                5.0%;
             4.3%; Score 45.6; DB 5.0%; Pred. No. 0.0057;
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 219; Mismatches
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.0031;
                          DB 1;
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                          Length 7218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Busfield,
                                                                                                                             TELEFAX: (617)742-421 INFORMATION FOR SEQ ID NO:
                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,2
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
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NAME/KEY:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                              LENGTH:
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                                                                                            746 base pairs
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No. 6197551el TANGO 80 Molecules and Uses Thereof
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                                                                                                                                       RESULT 5
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LENGTH: 1780
TYPE: DNA
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                                                                                              Sequence 5, Application US/08123934A Patent No. 6291206
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.1%;
Best Local Similarity 52.5%;
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                                                                  GENERAL INFORMATION: APPLICANT: WOZNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Government of the United States of America TITLE OF INVENTION: Fibroblast growth factor receptoractive TITLE OF INVENTION: related compositions and methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/202,548B CURRENT FILING DATE: 1998-12-15 PRIOR APPLICATION NUMBER: 60/020,009 PRIOR FILING DATE: 1996-06-18 PRIOR APPLICATION NUMBER: PCT/US97/10660 PRIOR FILING DATE: 1997-06-18 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (723)..(1487)
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                                      APPLICANT:
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           APPLICANT:
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NUMBER OF
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              INVENTION:
SEQUENCES:
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                          YAMAJI, No. 6291206oru
                                    THIES, R. Scott
                                                                  WOZNEY, John
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RECEPTOR PROTEINS
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Pred. No. 0.0093;
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Pred. No. 0.0061;
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                                                                                                                                                                                                                                                             Sequence 5, Application PC/TUDY911000:
GENERAL INFORMATION:
GENERAL INSTITUTE, INC.
APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEPHAX: 617 876 5851
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NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: HEREWITH
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
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CLONE: CFK1-10a
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CLASSIFICATION: 530
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                                                                                                                                                    COUNTRY: U.ZIP: 02140
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                                                                                                                                                                                                                  ADDRESSEE: Genetics Institute Inc. - Legal Affairs STREET: 87 CambridgePark Drive
CLASSIFICATION:
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Pred. No. 0.
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Best Local Similarity 69.0%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 110, Applica Patent No. 6261562 GENERAL INFORMATION:
               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
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                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                        MEDIIM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MADED: US/08/020 055
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 98104
                                                                                                                                                                               APPLICATION NUMBER: US/09 FILING DATE: 09-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                           STREET:
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LOCATION: 474
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STRANDEDNESS: single
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3410 base pairs
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870: 5:
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904 TGAATCACTGGAGCAAGCAGCCTACACCAAACGTGATGGAACACCCCCCAGGAGGGGGAAGA 963

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                                                             US-09-030-607-110
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    Matches
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                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3236
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
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ORIGINAL SOURCE:
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STREET: 50.
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                                                                                                                           TOPOLOGY:
                                                                                                                                        STRANDEDNESS:
                                                                                                                                                 LENGTH: 3410 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 Local Similarity
                                                                                                                                                                                                                               TELEPHONE:
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
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                                                                               ORGANISM:
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               3.98;
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 Score 42.2; DB 4;
Pred. No. 0.036;
1; Mismatches 69;
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                              Length 3410;
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Gaps
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; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-785-110
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                                                                                  Sequence 110, Application US/09439313 Patent No. 6329505
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                                                                     GENERAL INFORMATION:
           APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
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Best Local Similarity 54.2%;
Matches 83; Conservative
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210111.427C16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/605,785
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                                                                                                                                                                               1024 CCGAAAGTAAAAAAAAAAAAAAAAAAAAAAAAA 1056
                                                                                                                                                                                                                                                                    3236 TTATTTAGCGGGGGGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGG 3295
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Mitcham, Jennifer L.
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ick, Thomas S.
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Pred. No. 0.036;
1; Mismatches 69;
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APPLICANT:
APPLICANT:
1024 ССGARAGTARARARARARARARARARARARA 1056
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SOFTWARE: FASTSEQ for W. SEQ ID NO 110

LENGTH: 3410

TYPE: DNA

ORGANISM: Homo sapien
US-09-352-616A-110
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; ORGANISM: Homo sapien
US-09-439-313-110
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Best Local Similarity 54.2%;
Matches 83; Conservative
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR IT PROFERENCE: 210121.427C8
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR IT PROFERENCE: 210121.427C8
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Best Local Similarity 54.2%;
Matches 83; Conservative
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CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121,427C9
                                                                                   3236 TTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGG 3295
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TGGCAGCATTGCCTTTTATATTACGTTTTTATGGAAATGAACTGAAAAAAACTCTTGAAA 1023
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Reed, Steven G.
Kalos, Michael
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Retter, Mark
Solk, John
                                                                                                                                                                                  Conservative
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                                                                                                                                                                         Score 42.2; DB 4; Length 3410; Pred. No. 0.036; 1; Mismatches 69; Indels 0
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                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 338
SOFTWARE: FRATSEQ for Windows Version 3.0
SEQ ID NO 110
LENGTH: 3410
                                                                                                                                                 Query Match
Best Local
                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 100, Application US/09602877A Patent No. 6432707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2000-06-
NUMBER OF CON-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER FILE REFERENCE: 210121.446C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                      3236 TTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGG 3295
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964 TGGCAGCATTGCCTTTTATATTTATGGTTTTTATGGAAATGAACTGAAAAAACTCTTGAAA 1023
                                                                                       904 TGAATCACTGGAGCAAGCAGCCTACACCAAACGTGATGGAACACCCCCAGGAGGGGAAGA 963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 3.9%;
Local Similarity 54.2%;
les 83; Conservative
                                                                                                                              Local Similarity
es 83; Conserv
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Dillon, Davin C.
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Pred. No. 0.036;
1; Mismatches 69;
                                                                                                                          1;
                                                                                                                          Score 42.2; DB
Pred. No. 0.036;
1; Mismatches
                                                                                                                                                          DB 4; Length 3410;
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US-07-867-106-2/c
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                                                                                                                   Query Match 3.9%;
Best Local Similarity 70.9%;
Matches 56; Conservative
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TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: :
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APPLICANT: Slade,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & No. 5389526r1s
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                            1038 AAAAAAAAAAAAAAAAAA 1056
                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors f
TITLE OF INVENTION: Slime Moulds of the Genus
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                                                                                                                                                                                                                                 FEATURE:
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                                                                                     978 TTTATATTACGTTTTTATGGAAATGAACTGAAAAAACTCTTGAAACCGAAAGTAAAAAA 1037
                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
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CITY: P
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: 11r
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2378..5038
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Andy C
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Pred. No. 0.047;
0; Mismatches 23;
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s Dictyostelium
                                                                                                                                                Length 5852;
                                                                                                                     Indels
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RESULT 15 US-09-439-923-1

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Sequence 1, Application US/09439923
Patent No. 6426208
GENERAL INFORMATION:
APPLICANT: Emil D. Kakkis
APPLICANT: Emil D. Kakkis
APPLICANT: Emil D. Kakkis
TITLE OF INVENTION: For producing and Purifying the Same and Methods
TITLE OF INVENTION: Treating Diseases Caused by Deficiencies Thereof
CURRENT APPLICATION NUMBER: US/09/439,923
CURRENT APPLICATION NUMBER: US/09/439,923
CURRENT FILING DATE: 1999-11-12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 6200
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KBT: CDS
LOCATION: (1558)...(3516)
Search completed: March 30, 2003, 20:59:50 Job time: 104.294 secs
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Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 s
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length: 2000000000
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Match
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1069
     574371 seqs, 425486471 residues
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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                        US-10-028-072-173
US-10-121-049-173
US-10-123-904-173
US-10-140-470-173
US-10-176-918-173
US-10-176-918-173
US-10-176-918-173
US-10-176-921-173
US-10-137-865-173
US-10-140-474-173
US-10-140-474-173
US-10-140-002-173
US-10-142-419-173
US-10-142-419-173
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4.0	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.3	4.3	4.3	4.4	4.4	4.4	4.4	4.5	4.8	4.8	6.2	6.2	10.8	20.7
379	2272	963	745	745	687	687	1780	961	961	153	392	704	671	410	1260	444	444	444	416	126	126	147	147	281	564
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US-09-960-352-3105	US-09-796-753-11	US-10-023-896-17	US-09-764-855-13	US-10-072-349-13	US-09-969-730-107	US-09-774-639-106	US-09-942-858-5	US-09-764-846-98	US-10-091-483-98	US-09-768-827-42	US-09-960-352-2634	US-10-001-887-79	US-10-184-644-346	us-09-960-352-4438	US-09-893-737-105	US-09-764-846-34) US-09-764-869-533	US-10-091-483-34	US-09-960-352-4584	US-09-880-107-1334	US-09-954-456-778	US-09-880-107-1335	US-09-954-456-779	US-09-783-590-1551	US-09-864-864-228
Sequence 3105, Ap	Sequence 11 Appl	Secuence 17 April	Sequence 13. April	Sequence 13. Appl	Sequence 107. App	Sequence 106. App	Sequence 5. Appli	Sequence 98 Appl	Sequence 98. Appl	Sequence 42. April	Sequence 2634. An	Sequence 79. Appl	Sequence 346. App	Sequence 4438. An	Sequence 105. App	Sequence 34. Appl	Sequence 533. App	Sequence 34. Appl	Sequence 4584. An	Sequence 1334 An	Sequence 778. App	Sequence 1335. An	Sequence 779 App	Sequence 1551. An	Sequence 228, App

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR PRICIATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/05912
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PRICING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
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US-10-028-072-173
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Publication No
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APPLICANT:
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FILE REFERENCE:
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FILING
                 APPLICATION NUMBER:
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
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DATE: 1997-09-18
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		PRIOR	PRIOR	PRIOR	FILING DATE: 1998-01-23 APPLICATION NUMBER: 60/073612 APPLICATION NUMBER: 60/073612 FILING DATE: 1998-02-04 APPLICATION NUMBER: 60/074086 FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/074092	N NUMBER: 60 8: 1997-12-1 N NUMBER: 60 E: 1997-12-1: N NUMBER: 60 N NUMBER: 60 N NUMBER: 60	N NUMBER: 60 E: 1997-11-2 N NUMBER: 60 E: 1997-11-2 N NUMBER: 60 N NUMBER: 60	: 1997-1 NUMBER: : 1997-1 : 1997-1 : 1997-1	ATION NUMBER: 60 DATE: 1997-11-0 ATION NUMBER: 60 DATE: 1997-11-1 ATION NUMBER: 60	NUMBER: 60, : 1997-10-1: NUMBER: 60, : 1997-11-0:	: 1997-10-29 NUMBER: 60/06373 : 1997-10-29 NUMBER: 60/06373 : 1997-10-29	NOMBER: 60 1997-10-2 NUMBER: 60 1997-10-2 NUMBER: 60 1997-10-2	NUMBER: 60, : 1997-10-2: NUMBER: 60, : 1997-10-2: NUMBER: 60, : 1997-10-2:	1997-10-24 NUMBER: 60, NUMBER: 60, 1997-10-24 NUMBER: 60, 1997-10-3	DATION NUMBER: 60 DATE: 1997-10-1 ATION NUMBER: 60 DATE: 1997-10-1 ATION NUMBER: 60 DATE: 1997-10-2	: 1997-09 NUMBER: : 1997-09 NUMBER: : 1997-09 NUMBER: : 1997-10
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OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091982
OR FILING DATE: 1998-07-07
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R FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090538

DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090863

DR FILING DATE: 1998-06-26
CGAGGATGAGCTTATCGAATTCTTCTCCAGAGAGGCTGACAACGTTAAAGACAACTTTG
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                           AATTGACTCAGATATCAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAAGAATA
                                                              CTACGTACGCGTCGTGAGCCGGAATGGAGAATCCAGTGAACTAGACTTACAGGGCATCCG
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Pred. No. 1.7e-187;
0; Mismatches 145;
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
SEQ ID NO 173
LENGTH: 1210
                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapien
US-10-121-049-173
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Goddard, Audrey
Goddwski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Wood, William
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ilarity 84.4%;
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Pred. No. 1.7e-187;
0; Mismatches 145;
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RESULT 3
US-10-123-904-173

US-10-123-904-173

Sequence 173, Application
Publication No. US2003002:
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Berossini, Maur
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: GGO, Wei-Qiang
APPLICANT: GGO, Wei-Qiang
APPLICANT: Goodward, Audrey
APPLICANT: Goodward, Audrey
APPLICANT: Goodward, Nucrey
APPLICANT: Goodward, Audrey
APPLICANT: Sonith, Victoria
APPLICANT: Stewart, Tinoth)
APPLICANT: Stewart, Tinoth)
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETER
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Filvaroff, Ellen
Gao, Wel-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Gigurey, Austin L.
Fisherwood, Steven
Tisherwood, St
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o. US20030022328A1
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CURRENT APPLICATION NUMBER: US/10/123,90
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wra
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
ORGANISM: Homo Sapien
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                                                  AATCGACTCAGATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATA
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LLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TRANSMEMBRANE POLYPEPTIDES AND TRANSMEMBRANE POLYPEPTIDES AND FILLE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
PTIOT APPLICATION TEMOVED - See Palm - NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stevart, Timothy
APPLICANT: Stevart, Timothy
APPLICANT: Tumas, Daniel
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Best Local
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GENERAL INFORMATION
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                            -TAGTTTCGGGAGCCACTGGGGCCAAAGTGAGAGTCCAGCGGTCTTCCAGCGCTTGGGCC
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APPLICANT: Wood, WILLIAM
APPLICANT: Wood, WILLIAM
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RLC353
FILE REFERENCE: WIGHTH SAME
FILE REFERENCE: P3330RLC353
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 173, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin p. APPLICANT: Beresini, Maure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGGATGAGCTTATCGAATTCTTCTCCAGAGAGGCTGACAACGTTAAAGACAACTTTG
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                                                                                                                                              Tumas, Daniel
                                                                                                               Watanabe, Colin K
Wood, William
                                                                                                                                                              Stewart, Timothy A.
                                                                                                                                                                                   Smith, Victoria
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CURRENT FILING DATE: 2
Prior Application remov
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
ORGANISM: Homo Sapien
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llarity 84.48;
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NOS: 550
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; CURRENT FILLYG DATE: 2002-06-20
; Prior Application removed - See File Wrap
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 173
; SEQ ID NO 173
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-918-173
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US-10-176-918-173
; Sequence 173, App
; Publication No. 1
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APPLICANT: Goddard Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Chang, Zemin
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APPLICANT: Chang, Zemin
APPLICANT: Sherweller Second Audressen
APPLICANT: STATION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
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                           ACGCCGGCCCCTGGGAGCAGAGGTGGAGCGACCCCATTACGCTAAAGATGAAAGGCTG
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Similarity 84.4%;
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DeForge, Laura
Desnoyers, Luc
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o. US20030027275A1
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Pred. No. 1.7e-187;
0; Mismatches 145;
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APPLICANT: Barerion:
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Deforge, Laura
APPLICANT: Deforge, Laura
APPLICANT: Deforge, Laura
APPLICANT: Geno, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goodward, Audrey
APPLICANT: Goodward, Audrey
APPLICANT: Goodward, Paul J.
APPLICANT: Goodward, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: APPLICANT: SECTED AND TRANSMEMBRANE POLYPEPTIDES AND NUCL
TITLE OF INVENTION: SECTED AND TRANSMEMBRANE POLYPEPTIDES AND FILE REFERENCE: P3330R1C288
CUBRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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; SEO ID NO 173
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Homo S
US-10-176-921-173
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Best Local :
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CACTGGAGCAAGCAGCCTACACCCAAACGTGATGGAACACCCCCAGGAGGGGAAAGATGGCA 968
                                      CAGTAAGCGGACAGATCTATGTGACCATGCCCTGCACAGATCTCACGATGAGCTATGAAT 908
                                                                              CTACGTACGCGTCGTGAGCCGGAATGGAGAATCCAGTGAACTAGACTTACAGGGCATCCG
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Pred. No. 1.7e-187;
0; Mismatches 145;
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GCATTGCCTTT--TATATTACGTTTTTATGGAAATGAACTGAAAAAA 1013

GCAATGCCTTTTATATATATGTTTTTACTGAAATTAACTGAAAAAA 1195

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; LENGTH: 1210
; TYPE: DNA
; ORGANISM: HOMO S
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US-10-137-865-173
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Eller
APPLICANT: Gao, Wei-Qiang
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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Best Local Similarity
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT FILING DATE: 2002-05-03
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FILE REFERENCE: P3330R1C154
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                             GGGTTGGCTAGCCCTACTTTTGGGGGTCCTGCTGGGAACTGCCTGGGCTCGAAGGAGCCA 428
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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Pred. No. 1.7e-187;
D; Mismatches 145;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES /
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330781C162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
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                                                                                                                                                        Zhang, Zemin
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Watanabe, Colin K
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Godowski, Paul
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Gerritsen, Mary E.
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Filvaroff, Ellen
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o. US20030032156A1
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US-10-140-474-173
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Best Local
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                                  CGAGGATGAACTCATTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAAGACAAACTTTG
                                                                                                                             CGAGGATGAGCTTATCGAATTCTTCTCCCAGAGAGGCTGACAACGTTAAAGACAAACTTTG 848
                                                                                                                                                            AATTGACTCAGATATCAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGGAAGAATA
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Pred. No. 1.7e-187;
0; Mismatches 145;
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: SECRETED AND THE SAME
FILE REFERENCE: P3330R1C251
CURRENT APPLICATION NUMBER: US/10/142,431
CURRENT FILLING DATE: 2002-05-10
PRIOT APPLICATION TEMOVED
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
TYPE: DNA
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US-10-142-431-173
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                                                                                                                                                                                                                                                                                                                                    Query Match 64.6%;
Best Local Similarity 84.4%;
Matches 850; Conservative
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APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
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APPLICANT: Beresini, Ma
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                                      AGATCTACACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGAAATTGCCCG 488
                                                                               ACGGCGGCGGCCGTGGGAGCAGAGGTGGAGCGACCCTGTTACACTAAAGATGAAAGGCTG
                                                                                                                                     CTAGGGTTGGGACCCACAGAAAACAAAGTGAGAGTCCGGCTGCTTTCCAGAGCCTGGGCC
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Goddard, Audrey
Goddwski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Wood,William
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Length 1210;

12;

Gaps

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RESULT 11

US-10-143-114-173

Sequence 173, Application US/10143114

publication No. US20030036180A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: Gesneyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wel-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Stewart, Timothy A.

APPLICANT: Watanabe, Colin K

APPLICANT: Watanabe, Colin K

APPLICANT: Tumas, Daniel

APPLICANT: Stewart, Timothy A.

APPLICANT: Wood, William

APPLICANT: Shang, Zemin
                                      ; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC211
; CURRENT APPLICATION NUMBER: U5/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapi; NUMBER OF SEQ ID NO 173
; SEQ ID NO 173
; SEQ ID NO 173
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: HOMO
US-10-143-114-173
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Pred. No. 1.7e-187;
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RESULT 12 US-10-140-002-173

Sequence 173,

Application US/10140002 US20030037623A1

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; Prior Application removed - S; NUMBER OF SEQ ID NOS: 550; SEQ ID NO 173; LENGTH: 1210; TYPE: DNA; ORGANISM: Homo Sapien
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Best Local Similarity 84.4%;
Matches 850; Conservative
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APPLICANT: Beresini, Mau
APPLICANT: Desnoyers, Lu
APPLICANT: Desnoyers, Lu
APPLICANT: Desnoyers, Lu
APPLICANT: Gao, Wei - Qian
APPLICANT: Gerritsen, Ma
APPLICANT: Goddard, Audr
APPLICANT: Goddwski, Pau
APPLICANT: Godowski, Pau
APPLICANT: Gurney, Austr
APPLICANT: Sherwood, Ste
APPLICANT: Stewart, Timo
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-05-06
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Watanabe, Colin K
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DeForge, Laura
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Pred. No. 1.7e-187;
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; TYPE: DNA ; ORGANISM: Homo US-10-142-419-173

Sapien

Prior Apploication removed -NUMBER OF SEQ ID NOS: 550 SEQ ID NO 173 LENGTH: 1210

See File Wrapper

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Best Loc Matches

850;

Conservative

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Score 691; DB 9; Pred. No. 1.7e-187; 0; Mismatches 145;

Length 1210; Indels

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Query Match Best Local Similarity

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APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C244

CURRENT APPLICATION NUMBER: US/10/142,419

CURRENT FILING DATE: 2002-05-10
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Desnoyers, Luc
Filvaroff, Ellen
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Wood, William
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CURRENT FILING DATE: 2002-04-15
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
ORGANISM: Homo Sapien
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Best Local
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                   GGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCA 673
                                                                                                                                                     ACGCCGCCGCCGTGGGAGCAGAGGTGGAGCGACCCTGTTACACTAAAGATGAAAGGCTG 368
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                                                                           AGATCTACACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGGGAAATTGCCCCG
                                                                                                          GGGTTGGCTGGCTTCTGGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCA
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Tumas, Daniel
Watanabe, Colin K
Wood, William
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Pred. No. 1.7e-187;
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333ORIC249
CURRENT APPLICATION NUMBER: US/10/142,423
CURRENT FILING DAYE: 2002-05-10
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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                                                                                         ; TYPE: DNA
; ORGANISM: Homo
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APPLICANT: Beresini, Mau
APPLICANT: DeForge, Laur
APPLICANT: Desonyers, Lu
APPLICANT: Filvaroff, El
APPLICANT: Gao, Wei-Qian
APPLICANT: Godowski, Pau
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APPLICANT: Godowski, Pau
APPLICANT: Sherwood, Ste
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Matches
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Filvaroff, Ellen
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                                    Score 691; DB 9;
Pred. No. 1.7e-187;
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        GCATTGCCTTT--TATATTACGTTTTTTATGGAAATGAACTGAAAAAA 1013
                                 CACTGGAGCAAGCAGCCTACACCAAACGTGATGGAACACCCCCAGGAGGGGAAGATGGCA
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ALIGNMENTS

RESULT 1 AK019927 LOCUS REFERENCE AUTHORS ACCESSION VERSION KEYWORDS REFERENCE SOURCE DEFINITION JOURNAL MEDLINE PUBMED JOURNAL MEDLINE PUBMED TITLE ORGANISM TITLE AUTHORS Mus musculus Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; AK019927.1 GI:12860332
HTC; CAP trapper.
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male pituitary gland cDNA
mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
clone:5330432A10. Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000) Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253 AKO19927

Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330432AlO:transmembrane protein 4, full sequence. Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus new genes င် ៥

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REFERENCE
AUTHORS
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                   CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 3.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer
                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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                                                                                                                                                                                                                                                                                                                                                                         Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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146 AAGTGCGGGAAGCTGGGCCAGGCGGTCACTGGCCACCCTGAACCTGGCGGGAGCCGGAGC 205
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:5330432A10"
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        Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayyashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new components of the control of the control
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                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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Salto, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Salto, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Ouackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamotto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Havashizaki, Y. Oshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGCCCAGAGACCTCTTTTTTTTTTTTTTTVN 3'], CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                          Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Location/Qualifiers
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days embryo"

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Query Match
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                                                                                                                                                                  GCCGGAATGGAGAATCCAGTGAACTAGACTTACAGGGCATCCGAATTGACTCAGATATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCAGAGGTGGAGCGACCCTGTTACACTAAAGATGAAAGGCTGGGGTTGGCTAGCCCTAC 385
 TACACCAAACGTGATGGAACACCCCCAGGAGGGGAAGATGGCAGTTGCCTTTTATATT
                                                                                                                                 GCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAAGAATACGAGGATGAGCTTATCG
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                                                                                                                    GCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAAGAATACGAGGATGAGCTTATCG
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KNYVPKVSRNGESSELDLQGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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Matches 923; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tlssue Procurement: Lothar Hennighausen Ph.D., Robin Humphi
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11631 row: c column: 17
High quality sequence stop: 854.
Location/Qualifiers
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d'
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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/clone_lib="NCI_CGAP_Mam5"
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/dev_stage="7 months"
/lab_host="DH10B"
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/strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
1 (bases 1 to 856)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Ge
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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B1454180
B1454180.1 GI:
EST.
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hur
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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603170602F1 NCI_CGAP_Mam5
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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/tissue_type="tumor, gross
/dev_stage="7 months"
/lab_host="DH10B"
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/clone="IMAGE:5250001"
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Plate: LLAM11291 row: 1 column: 04
High quality sequence stop: 873.
Location/Qualifiers
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AAAACTCTTGAAACCGAAAAAACAAAACAACAAAATAA
                     AAAACTCTTGAAACCGAAAGTAAAAAAAAAAAAAAAAA 1049
                                                                                    TTAAAGACAAACTTTGCAGTAAGCGGACAGATCTATGTGACCATGCCCTGCACAGATCTC
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                                                                                                                                                                                   CTTACAGGGCATCCGAATTGACTCAGATATCAGCGGCACCCTCAAGTTTGCGTTGTGAGA
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REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM ACCESSION VERSION LOCUS DEFINITION RESULT 6 BI412341

COMMENT JOURNAL NIH-MGC http://mgc.nci.nih.gov/. national Institutes of Health, Mammalian Unpublished (1999) Contact: Robert Strausberg, Ph.D. BI412341 9 602991837F1 NCI_CGAP_Lu33 Mus musculus mRNA sequence. BI412341 Mammalia; Eukaryota; Metazoa; nouse mouse nmalia; Eutheria; (bases 1 to 945) cgapbs-r@mail.nih.gov Procurement: Gilbert GI:15173264 Chordata; Rodentia; 945 bp mRNA linear Mus musculus cDNA clone Smith, Craniata; Vertebrata; Sciurognathi; Muridae; Ph. Gene EST 14-AUG-2001 IMAGE:5147624 5', Euteleostom1;
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                                                                       CGAATCAATCCAGATGCAGCCAGTCAGTTGTGGAGGTACCTTATGCCCGCTCAGAGGCC
                                                                                     CGAATCAATCCAGATGGCAGCCAGTCAGTTGTGGAGGTACCTTATGCCCGCTCAGAGGCC
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TGACCCTTCTACCCACCGCAAGAACTACGTACGCGT-CGTGAGCCGGAATGGAGAATCCA
                        CACCTCACAGAGTTGCTTGAGGAGGTGTGTGACCGAATGAAGGAGTACGGGGGAACAGAT
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/strain="CZECH II"
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                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
MUS musculus (strain:C57BL/6J) 10
mRNA, clone_lib:RIKEN full-length
clone:1810060D19.
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Hara,A., Hayatsu,N., Hill,D., Hiramotc,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,K., Sano,H., Sasaki,D.,
Schrimi,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
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Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/strain="C57BL/6J"
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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carnioci,P., Fukuda,S., Fukuknishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F. Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 330-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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MY1_001606 Mouse 9-day fetus c

CDNA Clone ICRFD522B2440 5', m

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EST.
                                                                   Contact: Hennig S'
Laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare
Innestr.63-73, D-14195 Berlin, Germa
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
                                                                                                                     Mus musculus
Eukaryota; Metazoa;
                                                                                                                                    house mouse
: hennig@molgen.mpg.de
are made from clones being representatives of
clusters were calculated from oligonucleotide
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Seq primer: 5'-ATTTAGGTGACACTATAG-3'
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Location/Qualifiers
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/tissue_type="whole embryo"
/dev_stage="embryonic 9-day"
/lab_host="E.coli, XLI blue"
/note="vector: psvsport1; Site_1: Not1; Site_2: Sailbrary preparation by oligo_dT priming of RNA. Clibrary preparation by oligo_dT priming of RNA. Clibrary preparation by oligo_dT priming of RNA. Clibrary proparation by oligo_dT priming of RNA. Clibrary propagation by oligo_dT priming oligon by oligon by oligo_dT priming oligon by oligon b
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                                                      GCGGCGGCCGTGGGAGCAGAGGTGGAGCGACCCTGTTACACTAAAGATGAAAGGCTGGGG
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Mus musculus
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Plate: LLAM9525 row: n column:
High quality sequence stop: 685.
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Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN11293 row: n_column: 24
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; I
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae;
1 (bases 1 to 808)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectional Institutes of Health, Mammalian Insti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento
                                                                                                                                                                                                                                                                                                                                                             quality sequence start: 4 quality sequence stop: 768.
Location/Qualifiers
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5120471"
/clone_lib="NCI_CGAP_Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, Ph.D.
M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp mRNA linear EST 14-AUG-2001
s musculus cDNA clone IMAGE:5120471 5',
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GAAACCGAAAGTAAAAAAAAAAAAAAAAAA 1050
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                                                                                                                CAAACTTTGCAGTAAGCGGACAGATCTATGTGACCATGCCCTGCACAGATCTCACGATGA
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Pred. No. 3e-105;
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                                            GGGAACTGCCTGGGCTCGAAGGAGCCAAGATCTACACTGTGGAGCTTGCAGGGCTCTGGT
                                                                                                           CCCTGTTACACTAAAGATGAAAGGCTGGGGTTGGCTAGCCCTACTTTTGGGGGTCCTGCT
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                                                                                                                                                                                                                                                                                               GACAGCCCCGTTTTTCCCAGCCAGCTGCTAGGGTTGGGACCCACAGAAAACAAAGTGAGA 281
                                                                                                                                                                                                                                                                                                                                                                                        CCAGGCGGTCACTGGCCACCCTGAACCTGGCGGGAGCCGGAGCGCTC-TGGAGAAGCCGG 221
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                                                                                      CCCTGTTACACTAAAGATGAAAGGCTGGGGTTGGCTAGCCCTACTTTTGGGGGGTCCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humph.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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National institutes of Health, Mammalian
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Mammalia; Eutheria;
1 (bases 1 to 863)
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BI454899
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nilarity 96.5%;
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/clone="IMAGE:5252339"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross t.
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal: Site_2: Not1; Cloned unidirectionally. Primer: Oligo d'Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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/strain="C57BL/6J"
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Eutheria; Rodentia;
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                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Ge
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                       CAT--GCCCTGCACAGATCTCACGATGAGCTATGAATCACT-GGAGCAAGCAGCCTACAC
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602990995F1 NCI_CGAP_Lu33 Mus
                                                                              Plate: LLAM11362
                                                                                      found through the I.M.A.G.E. Consortium/ILNL http://image.llnl.gov
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                     BI412539.1
                                                                                                                                                                                                                                                                               mRNA sequence.
BI412539
                                                                                                                                                                                                                                                   house mouse
                                                                                                     cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by:Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution in
                                                  quality sequence start: 38 quality sequence stop: 824.
Location/Qualifiers
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/db_xref-"taxon:10090"
/clone-"IMAGE:5146967"
                                           . 843
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                                                                                                                                           Ph.D.,
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                           AGCAAGCAGCCTACACCAAACGTGATGGAACACCCCCAGGAGGGGAAGATGGCAGCATTG
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//tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_l: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5', TGTTACCAARCTGAASTGGGAGCGCCCCTCTGTTTTTTTTTTTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
39 a 195 c 238 g 171 t
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91.9%;
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                                             CGGCCGTGGGAGCAGAGGTGGAGCCACCCTGTTACACTAAAGATGAAAGGCTGGGG-TGG
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BI411532.1 GI:
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602965126F1 NCI_CGAP_Lu33
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Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/FLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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National Institutes of Health, Mammalian
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                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5120574"
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AGENCOURT 10050169 NIH_MGC_134 Mus
IMAGE:6508512 5', mRNA sequence.
B0963382
B0963382.1 GI:22378860
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 894)
                                                                                                                CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lnage.llnl.gov
Plate: LLAM14074 row: f column: 01
                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                      nouse mouse.
                                                                                                    quality sequence stop:
/clone="IMAGE:6508512"
/clone_lib="NIH_MGC_134"
/tissue_type="undifferentiated limb"
                                          /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                     ocation/Qualifiers
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                                      ACGAGGATG 674
                                                             AGATCTACACTGTGGAGCTTGCAGGCCTCTGGTGGATGAATTAGAGTGGGAAATTGCCCG
       ACGAGGATG 796
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/note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2:
NotI; Cloned unidirectionally. Primer: Oligo dT. Average
insert size 1.7 kb. Constructed by Resgen, Invitrogen
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Search completed: March 30, Job time: 1531.26 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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-Q-Ggn2_1/USPT0_spool_VS110082502/runat_24032003_135100_6599/app_query.fasta_1.1308
-Q-Ggn2_1/USPT0_spool_VS110082502/runat_24032003_135100_6599/app_query.fasta_1.1308
-DB-EST -QFMT-fastap -SUFFIX-rst -MINNATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blits -START-1 -END--1 -MATRIX-blosum62 -TRANG-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pot -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
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-NO_MARD -LARGEQUERY -NEG_SCORES-0 -WALT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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ALIGNMENTS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridao, Muriago, Muridao	Mus musculus	clone_lib:RIKEN full-length enriched mouse cDNA library clone:2900022B12.	Mus musculus (strain:C57BL/6J) adult male hippocampus cDNA to mRNA	HTC; CAP trapper.	AK013568.1 GI:12850979	AK013568	insert sequence.	enriched library, clone:2900022B12:transmembrane protein 4, full	ulus adult male hippocampus cDNA,	AK013568 754 bp mRNA linear HTC 19-JAN-2002		

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Direct Submission

Direct Submission

Direct Submission

Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute Submission (14 Sciences Center (6SC), RIKEN RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc:riken.go.jp, Kanagawa 20-0045, Japan (E-mail:genome-res@gsc:riken.go.jp, Tel:81-45-503-9222,
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/db_xref="GI:12850980"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                             Genome Res.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (strain:C57BL/6J) 10
mRNA, clone_lib:RIKEN full-length
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Hara, A. Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, J., Okido, T., Owa, C., Quackenbush, J., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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evidence: ISS

/note="data source:MGD,

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Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11293 row: n column: 24
High quality sequence start: 4
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Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Tissue Procurement: Gilbert Smith,
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Contact: Robert Strausberg,
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DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11362 row: n column: 24
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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Tissue Procurement: Gilbert !
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         Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new commerces. 10 (10), 1617-1630 (2000)
                                                                                                                High-efficiency
Meth. Enzymol
                                                                                                                                                                                                                        Mus musculus (strain:C57BL/6J) 10, 11 days clone_lib:RIKEN full-length enriched mouse
                                                                                                                                                                                                                                                                            Insert sequence
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20499374
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HTC; CAP trapper.
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Eutheria;
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ency full-length cDNA
ol. 303, 19-44 (1999)
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clone:2810406L24:transmembrane
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Rodentia;
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TE (bases 1 to 853)

RS Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Alzawa, K., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hune, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Szuwki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                     Shibata,K., Itoh,M., Alzawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:2810406L24"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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1255 bp mRNA linear HTC 19-JAN-20 Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330432A10:transmembrane protein 4, full
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S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Alzawa, K., Akahira, S., Fukunta, T., Aono, H., Bult, C., Carninci, P., Fukuda, S., Fukuntahi, Y., Furuno, M., Hanagaki, T., Alara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamanura, T., Yamanaka, I., Yasaunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                 /protein_id="Bab31921.1"
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KNYVPVSRNGESSELDLQGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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/db_xref="MGD:MGT:1899093"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                     transmembrane protein 4"
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/strain="C57BL/6J"
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l. .1255
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/clone_lib="RIKEN full-length
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E 1 (bases 1, Mennig, S., Neidhardt, L., Radelof, U., Hermann, B.G., Lehrach, H. and O'Brien, J.

Detection of a high number of novel genes in a 9-day mouse embryo cDNA library normalised by oligonucleotide fingerprinting

Unpublished (2001)
Unpublished (2001)
Lontact: Hennig S. laboraty 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inhestr. 63-73, D-14195 Berlin, Germany
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                         Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
EST's are made from clones being repre
Clone clusters were calculated from ol
PCR PRIMERS
FORWARD: 5'-GAGCTATTCCAGAAGTAGTGA-3'
BACKWARD: 5'-TAGTACGACTGATAGGG-3'
Seq primer: 5'-AATTAGGTGACACTATAGG-3'
High quality sequence stop: 802.
Location/Qualifiers
                                                                                                                                                                                                                                 GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
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/clone="ICRFp522B2440"
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/dev_stage="embryonic 9-day"
/lab_host="E.coli, XLI blue"
/note="Vector: PSVSport1; Site_1: NotI; Site_2: Sa:
Library preparation by oligo_dT priming of RNA. Cli
be ordered from the Resource Center in Berlin,
http://www.rzpd.de."
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http://image.llnl.gov
Plate: LLAM11291 row: 1 column: 04
High quality sequence stop: 873.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution informati
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
CDNA Library Preparation: M. Bent
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/strain="CZECH II"
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/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/clone="UI-R-DY1-coi-e-06-0-UI"
/clone_lib="UI-R-DY1"

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AUTHORS
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                                         Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8250
Email: msoareseblue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand CDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized cartilage library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
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                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ210416 724 bp mRNA linear EST 02-MAY: UI-R-DY1-coi-e-06-0-UI.sl UI-R-DY1 Rattus norvegicus cDNA clone UI-R-DY1-coi-e-06-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                           Contact:
                                                                                                                                                                                                                                                                                                               97044477
                                                                                                                                                                                                                                                                                                                                             discovery
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Bonaldo, M.F., Lennor
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BQ210416.1
                                 primer: M13
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US-10-082-502-19 (1-182) x BQ210416
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                                                                                               AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAsp 180
                                                                                                                                                                                                                                                                    CAGGGTATCCGAATCGATTCAGATATCAGTGGCACCCTCAAGTTTGCGTGTGAGAGCATT
                                                                                                                                                                                                                                                                                           GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle 140
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                                                                           GACAAACTTTGCAGTAAGCGGACAGATCTATGTGACCATGCCCTGCACAGATCTCATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-Porgan: Femur and Tibla; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; UI-R-DY1 is a normalized cDNA library containing the following tissue(s): Rat Cartilage from Femur and Tibla. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTAATGGACG. The Rat Cartilage tissue was provided by Dr Jeff Stevens at the TAG_LIB-UI-R-DYI
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TAG_SEQ-CTAATGGACG"
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/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim, N.S., Hahn, Y., Oh, Oh, K.J., Cheong, J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
1 (bases 1 to 588)
Kim, N.S., Hahn, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: yongsung@mail.kribb.re.kr
Plate: 11 row: B column: 03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21C Frontier Korean EST Project 2001 Unpublished (2002)
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                                                                                                                                                                                                                                                     /incte=-Norgan: Stomach; Vector: pTZ18RP1; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was decapped with tabacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOf' by electroporation method. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifue, the
                                                                                                                                                                subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells coll ToploF, with electroporation method."

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/cell_line="SNU-484"
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/clone_11b="S5SNU484s1"
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/db_xref="taxon:9606"
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E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. e
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                     Email: yongsung@mail.kribb.re.kr
Plate: 11 row: H column: 01
High quality sequence stop: 591.
Location/Qualifiers
                                                                                            Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4409

Fax: +82-42-860-4409
                                                                                                                                                               Genome Research Center
                                                                                                                                                                                 Unpublished (2002)
Contact: Kim YS
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Kin, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, Kim, Y.S.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/clone_lib="S5SNU484s1"
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similar to
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Inst Dept of Molecular and Cellular Biology, 7 Divi MA 02138
Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-8557
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                                                                     note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; CDNA made by oilgo-dT priming.
Size-selected on agarose gel. Average insert size -lkb. 5'
XhoI site was destroyed after directional cloning. Manplified once. Contact information: Hiroshi Inoue, MD, Methabolism Div. (Alan permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-7147-2692."
                                                                                                                                                                                                                                        /clone-"IMAGE:5085832"
/clone_lib="HR85 islet"
/tissue_type-"purified pancreatic islet"
/lab_host-"DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCTA
                                                                                                                                                                                                                                                                                                                     697 bp 602014708F1 NCI_CGAP_Brn64 Homo 5', mRNA sequence.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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EST.
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1 (bases 1 to 697)
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linear EST 22-NOV-2000 cDNA clone IMAGE:4150512

Gene Collection (MGC)

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/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH108 [T] phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Noti;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
73 a 167 c 220 g 137 t
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US-10-082-502-19 (1-182) x BE733900 (1-719)
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Best Local Similarity:
348 CATCGCANGAACTACGTACGTGTAGTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTA
                                                                                                                                                                                                                                                      21 ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                           | HisargLysasnTyrValargValValSerArgAsnGlyGluSerSerGluLewAspLeu
                                                                                                                                                                  AspGlySerGlnSerValValGluValProTyrAlaArgSerGluAlaHisLeuThrGlu 80
                                                                                                        LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr 100
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                                                                                 CTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGAACAGATTGATCCTTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nlh.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM537 row: k column: 18
High quality sequence stop: 710.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/tlssue_type="choriocarcinoma"
/tlssue_type="choriocarcinoma"
/lab_nost="DH10B (phage-resistant)"
/note="Organ: placenta; vector: poTB7; Site_1: xhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/xhoI sites using the following 5 adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CONA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
/clone="IMAGE:3843209"
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Query Match:
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1 (bases 1 to 742)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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602728454F1 NIH_MGC_15 Homo sapiens
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Dt10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
80 a 184 c 233 g 144 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4868100"
/clone_lib="NIH_MGC_15"
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/db_xref="taxon:9606"
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                                       GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle 140
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Search completed: March 31, 2003, 04:51:08 Job time : 1169.85 secs

Scoring table:

Minimum DB Maximum DB

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Title: Perfect score:

Run

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-Q-/cgn2_1/USPTO_spco1/US10082502/runat_24032003_135103_6870/app_query.fasta_1.1308
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-biosum62
-TRANS-human40.cdi -LIST-45 -DCCALICN-200 -TR_SCORE-pct -THR_MAX=100
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-NCPU-5 -ICPU-3 -NO_XMAP LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TREOUT-30 -THRANS-1 -SCAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-DEV_TIMEOUT-170 -WARN_TREOUT-30 -THRANS-1 -SCAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
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length: 2000000000
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

/cgn2_6/ptodata/2/pubpna/PCTUS.PUBCOMB.seq:*

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   Sequence 309, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
                                                                                        Description
APPLICANT: Lodes, Michaell J.
APPLICANT: Algate, Paul A.
APPLICANT: Filing, Steve P.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SOFTWARE: COrixa Invention Disclosure Database
LENGTH: 814
TYPE: DNA
ORGANISM: Homo sapiens
US-09-864-864-309
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 309, Application US/09864864 Patent No. US20020102679A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer
APPLICANT: Harlocker, Susan L
APPLICANT: Dillon, Davin C.
APPLICANT: Secrist, Heather
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US-10-176-918-173
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US-10-140-474-173
US-10-142-431-173
US-10-144-755-173
US-10-122-864-398
US-09-884-873-873-873
US-10-176-737-479
US-10-176-737-479
US-10-176-757-479
US-10-176-913-479
US-10-174-598-479
US-10-174-598-479
US-10-174-598-479
US-10-174-573-479
US-10-175-7743-479
US-10-175-7743-479
US-10-176-488-479
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Sequence 174, App
Sequence 228, App
Sequence 479, App
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Result No.

Score

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                       Sequence 173, Application
Publication No. US20030004
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P
APPLICANT: Beresini, Mauj
APPLICANT: DeForge, Laure
APPLICANT: DeForge, Laure
APPLICANT: Desnoyers, Luc
APPLICANT: Geo, Wei-Qian
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Audre
APPLICANT: Sherwood, Stee
APPLICANT: Sherwood, Stee
APPLICANT: Stewart, Timot
APPLICANT: Stewart, Timot
APPLICANT: Tumas, Daniel
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                                                                                                 Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Sherwood, Steven Smith, Victoria
                                                                                                                                                                                                                  DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
     Watanabe,Colin K
Wood,William
Zhang
                                                             Tumas, Daniel
                                                                             Stewart, Timothy A.
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DR FILING DATE: 1997-10-17
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R FILING DATE: 1997-12-11
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APPLICANT: Beresin; Maureer
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Mel-Qiang
APPLICANT: Gerritsen, Mary i
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CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper
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Gao, Wei-Qiang
Gerritsen, Mary E.
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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 US-10-082-502-19
                                                                                            Score:
                                                                                                            Pred. No.:
                                                                                                                                                       ; ORGANISM: HOMO US-10-123-904-173
                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Clang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Sharwood, Steven
APPLICANT: Sharwood, Steven
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapi
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 173, A Publication No.
                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C54
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                    LENGTH: 12
TYPE: DNA
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                        Wood, William
                                                                                                                                                                                                                                                                                                                                                                       Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                  Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beresini,Maureen
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(1-182) x US-10-123-904-173 (1-1210)
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Matches:
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; TYPE: DNA
; ORGANISM: Homo
US-10-140-470-173
   Alignment Scores: Pred. No.:
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                                                                                     SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Eller
APPLICANT: Gao, Mei-Qiang
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 7002-05-06
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 7002-05-06
CURRENT FILING DATE: 7002-06-06
CURRENT FILING DATE: 7002-06-06
CURRENT FILING 
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                       Prior Application removed NUMBER OF SEQ ID NOS: 550
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Wood, William
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Filvaroff, Ellen
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US-10-175-746-173
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DB:
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                                                                                                                                                                                                                                                                                                                               Sequence 173, Applic Publication No. US20 GENERAL INFORMATION:
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US-10-082-502-19 (1-182) x US-10-140-470-173 (1-1210)
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C353
                                                                                                                                                                                                           APPLICANT: Baker, Kevin p. APPLICANT: Beresini, MauraPPLICANT: Deforge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle
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                                                                                                                       Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                  Watanabe,Colin K
Wood,William
                                                                                                                                                       Gao, Wei-Qiang
Gerritsen, Mary E.
                                         Zhang, Zemin
                                                                          Tumas, Daniel
                                                                                     Stewart, Timothy A.
                                                                                                   Smith, Victoria
                                                                                                             Sherwood, Steven
                                                                                                                                                                                   Filvaroff, Ellen
                                                                                                                                                                                                        DeForge, Laura
                                                                                                                                                                                              Desnoyers, Luc
                                                                                                                                                                                                                      Beresini, Maureen
                                                                                                                                                                                                                                                       Application US/10175746 b. US20030027270A1
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; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Homo :
US-10-175-746-173
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Sequence 173, Application US
Publication No. US2003002727
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
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CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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        Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                             Application US/10176918 o. US20030027275A1
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 9330RLC382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
PILOT APPLICATION removed - See File Wrapper of
NUMBER OF SED ID NOS: 550
SEQ ID NO 173
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US-10-176-918-173
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy &
Tumas, Daniel
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Eller
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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Godowski, Paul J.
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; Prior Application removed - St; NUMBER OF SEQ ID NOS: 550; SEQ ID NO 173; SEQ ID NO 173; LENGTH: 1210; TYPE: DNA; ORGANISM: Homo Sapien
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
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CURRENT FILING DATE: 2002-05-03
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LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr
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                       GATGGCAGCCAGTCAGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAG
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Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
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APPLICANT: Beresini, Mau
APPLICANT: DeForge, Laur
APPLICANT: Desnoyers, Laur
APPLICANT: Filvaroff, El
APPLICANT: Gao, Wei-Qian
APPLICANT: Gerritsen, Ma
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CURRENT APPLICATION NUMBER: US/10/140,474
                                                                                                                                                                                                                                                                                                    Prior Application removed - NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-05-06
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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                                                                     SEQ ID NO 173
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CURRENT APPLICATION NUMBER: US/10/142,431
CURRENT FILING DATE: 2002-05-10
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APPLICANT: Beresini, Mau
APPLICANT: DePorge, Laur
APPLICANT: Desnoyers, Li
APPLICANT: Desnoyers, Li
APPLICANT: Gero, Wei-Qian
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APPLICANT: Goddard, Audz
APPLICANT: Goddwski, Pau
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APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 93390R1C211
CURRENT APPLICATION NUMBER: US/10/143,114
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                                                  Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K Wood, William
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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Sequence 173, Application
Publication No. US2003003
GENERAL INFORMATION:
APPLICANT: Baker, Kevin F
APPLICANT: Beresini, Mau
APPLICANT: DeForge, Laux
APPLICANT: Desnoyers, Lu
APPLICANT: Filvaroff, El
APPLICANT: Gao, Wei-Qian
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; ORGANISM: Homo
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Prior Application remov
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 173
LENGTH: 1210
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Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
                                   Deforge, Laura
Desnoyers, Luc
Filvaroff, Ellen
                                                              Beresini, Maureen
                                                                                         Application US/10140002 o. US20030037623A1
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Best Local Similarity:
Query Match:
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; ORGANISM: HOMO
US-10-140-002-173
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CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
PIOTA APPLICATION removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
ID NO 173
FERIOR OF SEQ ID NOS: 550
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                          GAGCTA
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                                                                      AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAsp 180
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                                                            GACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATGAT
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Percent Similarity:
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; ORGANISM: HOMO
US-10-142-419-173
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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CURRENT APPLICATION NUMBER: US/10/142,419

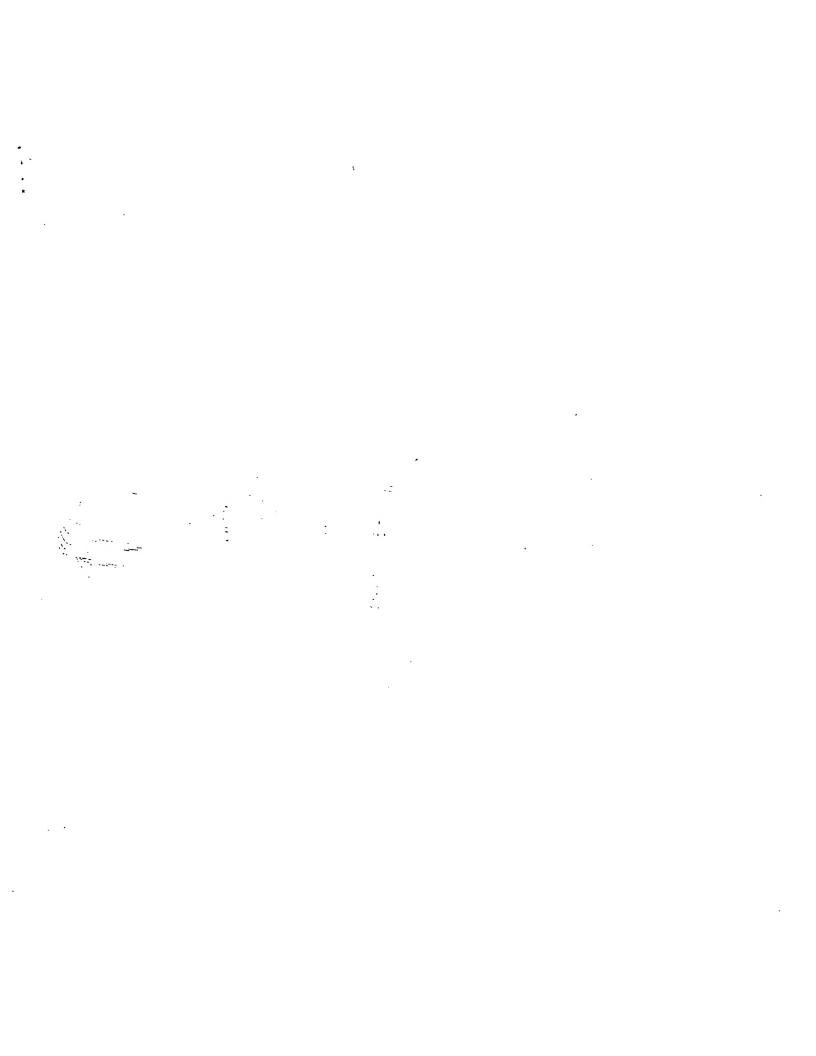
CURRENT FILING DATE: 2002-05-10
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ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
                                     GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
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Gurney, Austin L.
Sherwood, Steven
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Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
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; ORGANISM: Homo Sapien
US-10-123-262-173
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US-10-123-262-173
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LENGTH: 1210
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APPLICANT: Baker, Ke
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C38
CURRENT APPLICATION NUMBER: US/10/123,262
CURRENT FILING DATE: 2002-04-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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                                  LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
Sherwood, Steven
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Conservative:
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          GluLeu 182
                                                                 ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
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                               GACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATGAT
                                         AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAsp 180
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Search completed: March 31, 2003, 11:59:08 Job time: 59.0233 secs



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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlp
-O-/cgn2_flyST00_spool/US10082502/runat_24032003_135100_6616/app_query.fasta_1.1308
-OB-ISSUED_PATENTS_NA -OFMM-fastap -SUFFIX-rn1 -MINMATCH-0.1 -LOOPCL-0
-DB-ISSUED_PATENTS_NA -OFMM-fastap -SUFFIX-rn1 -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_KIN-0 -ALIGN-15
-MODE-LOCAL -OUTEMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXIEN-200000000
-USER-US10082502_@CGN_1_1_131_@runat_24032003_135100_6616 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WALT -LONGLOG -DEV_TIMEOUT-120
-MARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-0.5 -FGAPOD-6 -FGAPEXT-7
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is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-09-724-864-14

US-09-724-864-14

US-09-131-831B-2

US-09-131-831B-2

US-09-05-637-1

US-09-322-360-1

US-09-131-831B-1

US-08-316-231B-1

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US-08-69-99D-2

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Patent No. 6
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                                 TELEPHONE:
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	20, Āpp	Sequence 9, Appl1	1, Appl	e 1, Appl	e 1,	ω ·	e 103	e 42,	e 42,	42,	42, App	2	42, App	42, App	42,	<u>,</u>	208	159	Sequence 38, Appl	8	8	<u>38</u>	8,	8	38	e 38, App	2, Appl	62, App	1, Appl	۲	1, App	e 2, App	Sequence 2, Appli

ALIGNMENTS

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Sequence 3, Application US/09163285
Patent No. 6204013
GENERAL INFORMATION: APPLICANT: Khodadoust, Mehran
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTYWARE: PATENTIN BATA:
APPLICATION NUMBER: US/09/163,285
FILING DATE:
CLASSIFICATION NUMBER: US/09/163,285
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, ANY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-049
TELLECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
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Best Local Similarity:
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                                                                                                   Sequence 1, Application Patent No. 6204013
GENERAL INFORMATION:
                                               APPLICANT: Khodadous
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                       GluSerIleValGluGluTyrGluAspGluLeuIleGlu---PhePheSerArgGluAla 156
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                                                                                                                                                                                                   CAGCCCCTACAAAATTTTCTCTGT 552
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                                                           Khodadoust, Mehran
NVENTION: NOVEL MSP-5 PROTEIN
NVENTION: AND USES THEREOF
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Best Local Similarity:
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US-09-163-285-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E.
REGISTATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617),227-7400
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APPLICATION NUMBER: 60/0
FILING DATE: June 24, 19
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                            113 GlyGluSer-----SerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp 128
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                          GlnIleAspProSerThrHis-----ArgLysAsnTyrValArgValValSerArgAsn 112
                                                                                                                                                  AGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGGTGAAGGTGGATCTGGGG
                                                                                                                                                                                                CAGGTGCTG-----GATACAGGCAAGAGAGAGACACGTGCCTTACAGCGTTTCA
                                                                                                                                                                                                                                                                                          AspGluLeuGluTrpGluIleAlaArgValAsp---ProLysLysThrIleGlnMetGly
                                                                                                                                                                                                                                                                                                                              GAGGAGGACGATGACACAGAACGCTTGCCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGC 259
                                                                                                                                                                                                                                                                                                                                                                                             TTGGGAATATTGCTTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAG
                                                                                                                               GAGACAAGGCTGGAAGAGCCTTAGAGAATTTATGTGAGCGGATCCTGGACTAT-----
                                                                                                                                                                                                                             SerPheArgIleAsnProAspGlySerGlnSerValValGluValProTyrAlaArgSer
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LENGTH: 915
TYPE: DNA
ORGANISM: MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Polynucleotides, polypeptides expressed TITLE OF INVENTION: by the polynucleotides and methods for their use. FILE REFERENCE: 11000,105001

CURRENT APPLICATION NUMBER: US/09/724,864

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

PRIOR PILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                86
                                                                                                                                                                                                   66 ValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluVal 85
                                                                                                                                                                                                                                                                46 AspProLysLysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSer 65
                                                                                                                                                                                                                                                                                                                             26 LeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaArgVal 45
                                                                                                                                                                                                                                                                                                                                                               98 TCGGCTTCGGCTCCCACACTGGATGATGAAGAAGTACTCGGCTCATATGCCGGCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                             38 CTGTTGCTACTGTTCGGGTGCAGGGCTATCCTGGGGAGCGCCGGGGATAGGGTTTCCCTC
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                                       CAGATGAAGCGTCTCACGGGCCCAGGACTTAGCAAGGGGGCCAGAG------CCAAGA
      IleAspSerAspIleSerGly------ThrLeuLysPheAlaCysGluSer 139
                                                                     TyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArg
                                                                                                                                    CysAspArg---MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsn
                                                                                                                                                                                                                                 GAGGCTAAATCTCAC-----GGA 250
                                                                                                              TGCTCTCAGAACTGGCAGTCCTATGGA--
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Matches:
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                    Query Match:
                                       Percent Similarity:
Best Local Similari
                                                                   Score:
                                                                                                Alignment Scores:
                                                                                                                                  US-08-257-073-10
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APPLICATION NUMBER: US 0
FILING DATE: 20 MAR-1991
                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
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FILING DATE: 11-JUN-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 08/075,783
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
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APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 143
                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0'
FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 09-JUN CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                Similarity:
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425066 CURTMS
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GENERAL INFORMATION:
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                 COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WOOTSDET foct
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,831B
FILING DATE: 11-Aug-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/809,999
FILING DATE: 9-April-1997
APPLICATION NUMBER: 08/316,231
FILING DATE: 90-September-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 639149man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5386.3
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette, 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Coulie, Pierre; Ikeda, Hideyuki; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules
Coding For Tumor Rejection Antigen Precursors DAGE
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GATTATGAAAAGTCAAAAAAGGATTATGAAGAATTACTTGAAAAATTTTATGAAATGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATATGGTGATTTAATGAATCCTGATACTAAAGAAAAATTAATGAAAAAATTATTACA 1431
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STATE: New York
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DB:
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Best Local Similarity:
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                                                                                         Sequence 1, Application US/08809999D Patent No. 6013765
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
 APPLICANT: Coulie, Pierre APPLICANT: Boon-Falleur, TITLE OF INVENTION: Isola TITLE OF INVENTION: Codding INTERIOR INVENTION: Uses
                                                                                                                                                                                                              715
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STRANDEDNESS: double
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lleur, Thierry
Isolated Nucleic Acid Molecules
Coding For Tumor Rejection Antigen
Uses Thereof
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Matches:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5386.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/316,231
FILING DATE: 30-September-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6013765man D.
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,999D
FILING DATE: 9-April-1997
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MEDIUM TYPE: Diskette,
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STRANDEDNESS: double
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OPERATING SYSTEM:
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                                                                                                                                                   AACTCTCATCAGGACTTCTGGACTGTATGGTCTGGAAACAGGGCCAGTCTGTACTCATTT
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ValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsn 104
                                                         ValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGlu---
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666 Fifth Avenue
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12) 752-5958
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RESULT 7
US-09-069-637-1
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                                            Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-082-502-19 (1-182) x US-09-069-637-1 (1-1554)
                                                                                                                        Alignment Scores:
                                                                                                         Pred. No.:
                                                                                                                                                      US-09-069-637-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6022692
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                       TELEFAX: (212) 838-388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 9-April
APPLICATION NUMBER:
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-Septembe ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules
TITLE OF INVENTION: Coding For Tumor Rejection Anti:
                                                                                                                                                                                                  MOLECULE TYPE:
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MEDIUM TYPE: Diskette,
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                                                                                                                                                                                                                                                                                                                                                 NAME: Hanson, No. 602269
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
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OPERATING SYSTEM:
                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                  TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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STATE: New York
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PR: LUD 5386.1
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 8
US-09-322-360-1
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette,
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                    ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS
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                                                                                         CLASSIFICATION:
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E: New York
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   Hanson,
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Rejection Antigen Precursors
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Best Local Similarity:
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                                Sequence 1, Application US/09131831B Patent No. 6339149
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: URFERENCE/DOCKET NUMBER: UTELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
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TOPOLOGY: 11r
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                  APPLICANT:
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Coulie, Pierre; Ikeda, Falleur, Thierry
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DB:
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Best Local Similarity:
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TELEPHONE: (212) 318-3100
TELEFAX: (212) 318-3400
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
     498 CCAGAGCCAGAAGCAGCTCAGCCCATGACAAAGAAGCGAAAAGTAGATGGTTTGAGCACA
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APPLICATION NUMBER: 08/809,999
FILING DATE: 9-April-1997
APPLICATION NUMBER: 08/316,231
FILING DATE: 30-September-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: DAGE (5E10)
SEQUENCE DESCRIPTION: SEQ ID
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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ADDRESSEE: Fulbright & Jaworski L.L.P.
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                                                                   NACTCTCATCAGGACTTCTGGACTGTATGGTCTGGAAACAGGGCCAGTCTGTACTCATTT
                                                                                                                                   CTCCTTGCCCAGGAGGTTCGCCCCAGGAGGTGGAAACTTCAAGTGCTGGATTTACGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/131,831B FILING DATE: 11-Aug-1998 CLASSIFICATION: 435
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 666 Fifth
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Coding For Tumor Rejection Antigen Precursors DAGE and
Uses Thereof
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                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/316,231B FILING DATE: 30-September-1994 CLASSIFICATION: 536 ATTONNEY/AGENT INFORMATION: NAME: Hanson, No. 5830753man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: 10D 5386 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                              TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Isolated Nucleic Acid Molecules
TITLE OF INVENTION: Coding For Tumor Rejection Antigen Precursors DAGE and
TITLE OF INVENTION: Uses Thereof
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM:
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                                                                                                                  OTHER INFORMATION:
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US-08-809-999D-2
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                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08809999D Patent No. 6013765
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Coulie, Pierr
APPLICANT: Boon-Falleur,
                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                     NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski,
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                         STREET: 666 Fifth AVCITY: New York City
STATE: New York
              APPLICATION NUMBER: US/08/809,999D FILING DATE: 9-April-1997 CLASSIFICATION: 435
                                                                                                                                              COUNTRY: USA
ZIP: 10103
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                                                                                                                                                                                                                                                                                                                                Coulie, Pierre; Ikeda, Hideyuki;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GATATCAAGATGATCCTGAAAATGGTGCAGCTGGACTCTATTGAAGATTTG 774
                                                                                                                                                                                                                                                                    Isolated Nucleic Acid Molecules
Coding For Tumor Rejection Antio
Uses Thereof
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US-09-069-637-2
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 6013765man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 53
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2148 base pairs
TYPE: nucleic acid
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FILING DATE: 30-September-1994
ATTORNEY/AGENT INFORMATION:
                                                                    950
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---aagggacaacatcttcacctggagaccttcaaagctgtgcttgatggacttgatgtg
                                                                                                                                                      IleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIleValGluTyr 144
                                                                                                                                                                                                                               TyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArg
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                                                                                                                                                                                                                                                                                                                              ValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGlu---
                                                                                                                                                                                                                                                                                                                                                                                             CCAGAGCCAGAAGCAGCTCAGCCCATGACAAAGAAGCGAAAAGTAGATGGTTTGAGCACA
                                                                                                                                                                                                  GTACTACGCCTGTGCTGAAGAAGCTGAAGATTTTTTGCAATGCCCATGCAG------
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212) 752-5958
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84.00
38.67%
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Matches:
Conservative:
Mismatches:
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Gaps:
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2, Application US/09069637

Patent No. 6022692

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US-10-082-502-19 (1-182) x US-09-069-637-2 (1-2148)
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DB:
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US-09-069-637-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/809,999
FILING DATE: 9-April-1997
APPLICATION NUMBER: 08/316,231
FILING DATE: 30-September-1994
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 6022692man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
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                                      614 AACTCTCATCAGGACTTCTGGACTGTATGGTCTGGAAACAGGGCCAGTCTGTACTCATTT
                                                                                                     554 CTCCTTGCCCAGGAGGTTCGCCCCAGGAGGTGGAAACTTCAAGTGCTGGATTTACGGAAG
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CURRENT APPLICATION DATA:
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APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules
TITLE OF INVENTION: Coding For Tumor Rejection Antigen Precursors DAGE and Uses
                    57
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                           ThrileGlnMetGly----
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                                                                                                                               ----TrpGluIleAlaArgValAspProLysLys 49
                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
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          ---ArgIleAsnProAspGlySerGlnSer 65
                                                                      ----SerPhe 56
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                                                    ; NAME/KEY: US-09-322-360-2
                  Alignment Scores:
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US-09-322-360-2
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                                                                                                                                                                           TELEPHONE: (212) 318-3
TELEFAX: (212) 752-595
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Coulie
                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION: TELEPHONE: (212) 318-3000
                                                                                               MOLECULE TYPE:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
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TOPOLOGY: 11
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OPERATING SYSTEM:
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                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                        NAME: Hanson, NO. 6: REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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STATE: New York
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6297050
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666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                               DAGE (H12)
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                                                                                               nucleic acid
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lleur, Thierry
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Coding For Tumor Rejection Antigen Precursors DAGE and
Uses Thereof
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Length:
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Sequence 2, Application US/09103840A

Patent No. 6294328

Patent No. 6294328

REPLICANT: FELISCHAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION UNMER: US/09/103,840A

CURRENT APPLICATION NUMBER: US/09/103,840A

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Search completed: March 31, 2003, 04:26:04 Job time : 1346.68 secs
Qy 162 LysLeuCysSerLysArgThrAspLeuCysAspH1sAla 174 Db 4389595 GCGTTGGCTGCGGAGATCACCGCGGTGGTGTCGCACGCC 4389557
Oy 149IleGluPhePheSerArgGluAlaAspAsnValLysAsp 161 :::::: Db 4389643 GCCCATGACATCGCGGTGGTGGTCGACCAGTTCAGCGGGGAAGTGGAC 4389596
Qy 132 ThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeu 148
Qy 112 AsnGlyGluSerSerGluLeuAspLeuGlnGlyIleAsqIleAspSerAspIleSerGly 131 ::::::
Oy 92 TyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgValValSerArg 111
Qy 75 GluAlaHisLeuThrGluLeuLeuGluGluValCysAspArgMetLysGlu 91
Qy 55 SerPheArgIleAsnProAspGlySerGlnSerValValGluValProTyrAlaArgSer 74
Qy 41GluIleAlaArgValAspProLysLysThrIleGlnMetGly 54 :::
Qy 22ArgSerGlnAspLeuH1sCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp 40 ::
Oy 2 LysGlyTrpGlyTrpLeuAlaLeuLeuGlyValLeuLeuGlyThrAlaTrpAlaArg 21
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Score	% Query Match	Length	DB	SUMMARIES	Description
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938	97.8	806 806	20	AAX38326 AAX06969	
938	7.	0	21	AAZ08293	Secret
938	97.8	814	21	AAZ38327	Human transmembran
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889	Ņ	832	20	AAX97837	Human secreter
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Mouse secretory peptide-9 (2sig9) orthologue cDNA. Secretory peptide-9; Zsig9; orthologue; mouse; tumour marker; cancer; therapy; diagnosis; growth enhancer; ss. 10-MAY-1999 AAX06970 standard; cDNA; 1069 (first entry) Location/Qualifiers 358..906 BP.

ALIGNMENTS

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                                                                                                                                                                                                                                                                                  This cDNA clone encodes novel mouse secretory peptide-9, or zsig9 (see AAW88476), an orthologue of novel human zsig9 (see AAW88469). It luman zsig9 is overexpressed in a number of tumours including brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors, and thus can be used as an indicator for cancer. The invention provides polynucleotides (see AAW88469-70) encoding zsig9 polypeptides (see AAW88469-77) including mature polypeptides, other processed forms, variants and the mouse orthologues. The zsig9 gene, or probes derived from it, can be used to determine if zsig9 is present on chromosome 10, and if a mutation has occurred. Antibodies raised against zsig9 can be used as diagnostic agents to determine the presence of zsig9, and thus the presence of cancer. They can also be labelled with this the presence of cancer. They can also be labelled with zadioisotopes or fused with toxins and used to treat tumours which overexpress zsig9. Antisense nucleotides derived from zsig9 collar and so be used to inhibit the growth of tumour cells. Zsig9 proteins can be used to enhance the growth or development of the
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03-JUL-1997;
03-JUL-1997;
19-MAY-1998;
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therapeutic;
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                                   Moore
                                                   (ZYMO ) ZYMOGENETICS
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                                                                                                                                                                                                                                                                                                                      Mouse ortholog
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                       AAZ38326 standard;
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GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro

ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp

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60 20

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CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGG

MetLysGlyTrpGlyTrpLeuAlaLeuLeuClyValLeuLeuGlyThrAlaTrpAla

Best Local Similarity: Query Match:
DB:

Percent Similarity:

9.09e-100 938.00 98.35% 97.25% 97.81%

Length:
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Conservative:
Mismatches:
Indels:
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Alignment Scores:

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Sequence

546 BP;

139 A; 126 C;

165 G; 116

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0 other;

US-10-082-502-19 (1-182) x AAZ38326 (1-546)

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This sequence represents the coding sequence of human cDNA clone HP10390 which encodes a 20 kD protein with one putative transmembrane domain in the N-terminus. The cDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically.
                                                                                                                                                                                                                                            Human proteins with transmembrane domains, inv
proliferation and differentiation, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HP10390; transmembrane domain; stomach cancer cell; antibody; assay reagent; diagnostic marker; primer; probe; antisense; gagonist; antagonist; ligand; therapeutic; ds.
                                                                                                                                                                                                   Claim
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(PROT-)
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                                                                                                                                                                                                                                                                                                                                Kimura
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"No stop codon given in the specification"
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AspGlySerGinSerValValGluValProTyrAlaArgSerGluAlaHisLeuThrGlu 80 GAAATTGCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCA

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19-MAY-1998;
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17-JUN-1998;
      P-PSDB;
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               WPI; 1999-106055/09.
                              Jaspers
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                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                  Secretory peptide-9; Zsig9; human; tumour marker; cancer; therapy; diagnosis; growth enhancer; variant; ss.
                                              (ZYMO ) ZYMOGENETICS
                                                                                                                                      14-JAN-1999
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                         Human secretory peptide-9 (Zsig9) variant cDNA.
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                              SR,
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                              Jelinek
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                                                             98US-0099005.
97US-0051704.
97US-0888088.
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Claim 2;
                                                                                                                           New mammalian secretory peptide-9 (Zsig9) - used as a growth enhancer for placenta, liver and heart, and as an indicator of
                                                                                                            Page 73-74; 85pp; English
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This cDNA clone encodes human secretory peptide-9, or zsig9, cvariant (see AAW88474). Zsig9 (see also AAW88469) is overexpressed in chuman brain, liver, lung, oesophageal, stomach, colon, rectal, cthyroid and lymphoma tumors. Thus, Zsig can be used as an close from a full-term pregnancy cDNA library which contained an cc clone from a full-term pregnancy cDNA library which contained an cc expressed sequence tag (see AAX06971). The invention provides comply contained an cc expressed sequence tag (see AAX06971). The invention provides (see AAW88469-77) including mature polypeptides, other processed forms, cc variants and mouse orthologues. The zsig9 gene, or probes derived cc from it, can be used to determine if Zsig9 is present on chromosome cl 2, and if a mutation has occurred. Antibodies raised against cc zsig9 can be used as diagnostic agents to determine the presence of csig9, and thus the presence of cancer. They can also be labelled with radioisotopes or fused with toxins and used to treat tumours c which overexpress zsig9. Antisense nucleotides derived from zsig9 c cNA can also be used to enhance the growth or development of the proteins can be used to enhance the growth or development of the proteins can be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also be used to enhance the growth or development of the cx can also can be used to enhance the growth or development 'n

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643		584	Дb
180	AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAsp	161	Qy
583		524	ДЬ
160	ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys	141	Qy
523	CAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATT	464	ρb
140		121	Qy
463	-	404	Вb
120	HisArgLysAsnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu	101	Qy
403		344	망
100	LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnTleAspProSerThr	81	φ
343	GATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAG	284	뮍
08		61	Qy
283		224	D
60	GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro	41	Qy
223		164	рь
40	ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp	21	Qγ
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                                    The present DNA sequence is a gene encoding the variant of the secretory protein-9, Zsig9 that arises due to alternative splicing, allelic variation or silent mutations that result in amino acid changes. This sequence is mapped to the human chromosome 12q15 region. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to Zsig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to Zsig9 and it may be radio-regulating the overexpression of Zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding Zsig9. The Zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma, etc., at an early stage.
     Sequence 806
                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting tumors using antibodies, nucleotides to secretory protein-9
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 33-35;
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     B₽;
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/product= "Zsig9 secretory protein
/note= "Overexpressed in tumours"
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Alignment Scores

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                                                                                      HP10390; transmembrane domain; stomach cancer cell; antibody; assay reagent; diagnostic marker; primer; probe; antisense; gagonist; antagonist; ligand; therapeutic; ds.
                                                                                                           нр10390;
                                                                                                                          Human transmembrane
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the human cDNA clone HP10390 which encodes a 20 kD protein with one putative transmembrane domain in the N-terminus. The cDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human proteins with transmembrane domains, proliferation and differentiation, useful inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 106-107; 114pp; English.
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ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
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DB; AAY52391.
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Mismatches:
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11-0CT-2000;
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11-0CT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed cytotoxic
                                                                                                                            Identifying modulators of a cancer-related gene to screen agents for preventing or treating cancer comprises detecting a difference in the expression of cancer-linked genes in the presence or absence of test compounds
                                                                                                                           compounds
                                                                                                                                                                        P-PSDB;
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P-PSDB; AAU97063.
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T lymphocyte; chemotherapy; cytos;
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2000US-239605P
2000US-239805P
2000US-239805P
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The invention relates to modulators of a cancer-related genes. Also described are: (1) processes for identifying an anti-neoplastic agents comprising contacting a cell exhibiting neoplastic activity with a compound first identified as a cancer related gene modulator, and detecting a decrease in the neoplastic activity. (2) a process for determining the cancerous state of a cell by determining an increase in the level of expression of at least one gene, where an elevated expression relative to a known non-cancerous cell indicates a cancerous state or potentially cancerous state. The anti-neoplastic agent is useful for treating cancer or for protecting an animal against cancer. The immunogenic composition is also useful for treating cancer in an

Claim 1; Page 43; 66pp; English.

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RESULT 8
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                            Antibody; antigen;
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                                                                      11-JUN-2002
                                                                                           ABL41995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animal, where the composition elicits the production of cytotoxic T lymphocytes specific for the immunogenic composition. Preferably, the animal is a human. The cancer-linked genes and polypeptides are also useful as targets for cancer therapy or chemotherapy. The present sequence represents a cancer-linked gene located on chromosome 12, which encodes transmembrane protein 4.
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                                                                                                                                                                                                                                                                  No.:
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cc polypeptide comprising a portion of an ovarian tumour protein. The cc sequences of the invention are useful for stimulating an immune response cc and for treating ovarian cancer in a patient. An antigen presenting cell that expresses the sequences is useful for treating ovarian cancer by c incubating CD4+ and/or CD8+ T cells isolated from a patient. The T cells can then be proliferated and administered to the patient to inhibit the cc development of cancer. The DNA sequences are useful as probes or primers cf for nucleic acid hybridisation, to direct expression of a polypeptide in appropriate host cells. Detecting the presence of a cancer in a patient clivolves obtaining a biological sample from the patient, contacting the biological sample with an agent that binds to the protein, detecting the growthin to a predetermined cut-off value and determining the presence of cancer. Sequences ABK09464-ABK09802 represent PCR primers and CDNA cc molecules encoding ovarian tumour proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                       CC The invention relates to nucleic acid sequences (AAX22111 to AAX22134) CC encoding human secreted proteins (AAY01158). The secreted CC protein gene sequences are deposited with the ATCC under deposit number CC ATCC 209118. Host cells comprising recombinant vectors containing the CC acid sequences are used for the recombinant production of the CC conditions e.g. The polynucleotide and amino acid sequences are useful CC conditions e.g. by protein or gene therapy. Pathological conditions can CC sample or by determining the amount of the mew polypeptides in a CC polynucleotides. Dased on which tissues they are most highly expressed CC in, and include developing products for the diagnosis or treatment of caneer, tumours, developmental abnormalities and foetal deficiencies, schizophrenia, immunological disorders, and cognitive disorders, caneer, tumours, developmental abnormalities and foetal deficiencies, schizophrenia, immunological disorders, immune deficiency diseases (AIDS), mood disorders, respiratory disorders, arthritis, asthma, CC disorders or gastrointestinal disorders, skeletal disorders, cardiovascular disorders, endocrine contentifying their binding partners. The polypeptides are also useful gene encoding a human secreted protein (see descriptor line for gene
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12-SEP-1997;
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                       GACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATGAT
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22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
10-NOV-2000;
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PRO
PRO
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LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr
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DB; AAU12258.
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2000WO-US14042.
2000WO-US14941.
2000WO-US15264.
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A, Godowski PJ, Gurney ;
Tumas D, Watanabe CK, W
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                                               AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAY36129-Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies
Sequence
                              capable of binding to diagnostic, forensic,
                                                                                                   Claim 1;
                                                                                                                        Extended
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13-APR-1998;
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therapy; chromosome
                    design
                   to the secreted proteins. They may also be used in ic, gene therapy and chromosome mapping procedures. design of expression vectors and secretion vectors.
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                                                                                                                                                                            Human secreted protein; hyperproliferative disorder; autoimmune disorder immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene;
06-APR-2000; 2000US-195605P
                                       29-MAR-2001;
                                                                                                                                                                                                                                                                                              cDNA sequence #398 encoding novel human secreted
                                                                             18-OCT-2001
                                                                                                             WO200177289-A2
                                                                                                                                                  Homo sapiens.
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Merberg D, Clark HF, Jacobs K, Merberg D, WPI; 2002-179322/23 Fechtel K, мссоу лм, Lavallie ER
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, Howes SH, e ER, ino MJ, Bowma.. °ч, Resnick RJ, Collins-Racie LA, Evans Bowman MR, Spaulding V, Bownick RJ, Gulukota K, G Graham Ç Wong GG; raham JR;

Six hundred and twenty three polynucleotides derived from a human tissue sources which encode secreted proteins, useful treating immune deficiencies and disorders such as autoimmur autoimmune variety for disorders

Claim 1; Page 297; 393pp; English.

The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been content of the con proteins.

Sequence 657 B₽; 177 A; 149 C; 185 ç 146 T; 0 other;

Alignment s Pred. No.: Percent Similarity:
Best Local Similarity:
Query Match:
DB: Score: Scores: 8.91e-95 896.00 97.19% 95.51% 93.43% Length:
Matches:
Conservative:
Mismatches:
Indels: 170 170 3 0

US-10-082-502-19 (1-182) x ABK36007 (1-657)

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13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                        AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAY36129-Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.
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21 ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGlu-LeuGluTr
                                                                        MetLysGlyTrpGlyTrpLeuAlaLeuLeuLeuGlyValLeuLeuGlyThrAlaTrpAla
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Human; mouse; chicken; rat; secreted expressed sequence tag; SEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; analgesic; haemostatil thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoprosis; osteoarthritis; central nervous system disorder; Alzheimer; s disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                 Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc sequence tags (SESTS), isolated from human, mouse, chicken and rat Ctissue sources. The SESTS can have a range of activities depending on the second content of the tissues they were isolated from. The activities depending on chemotactic; proliferative; immunomodulatory; haematopoletic; chemotactic; antipacterial; antifungal; antiviral; antidiabetic; cytostatic; antipacterial; antilpropal; antiviral; antidiabetic; cytostatic; unlarrary; antilpropal; antiviral; antidiabetic; conciropic; antiparkinsonian; antipsoriatic; cerebroprotective; conciropic; antiparkinsonian; antipsoriatic; cerebroprotective; canticonvulsant; and antidepressant. The SESTs can be used for gene conciropic; antipactions of full-length cDNAs and genomic DNA concludes which correspond to the SESTs. Proteins encoded by the SESTs care useful as probes for the concludes which correspond to the SESTs. Proteins encoded by the SESTs care useful as genomic DNA concludes which correspond to the SESTs. Proteins encoded by the SESTs care useful as activity and raising concludes. They may be useful for treatment of autoimmune disorders continuity becomes a conditions. CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, csteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation constants. ANA45926 to ANA45931 represent linker variants which are given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 228-229; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
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                                                                             rHisArgLysAsnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLe
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Command line parameters:

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-O-/cgn2_1/USPTO_spool/US10082502/runat_24032003_135059_6547/app_query.fasta_1.1308
-DB-GenEmbl -QFMT-fastap -SUFFIX-rge -MINMATCH-0.1 -LOOPCLO -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MARRIX-blosum62 -TRANS-human10.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-UNITMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US10082502_eCGN_1_1_4/58_erunat_24022003_135059_6547 -NCPU-6 -ICPU-3
-NO_XLEXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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                   March 30, 2003, 22:24:04; Search time 1725.3 Seconds (without allgaments) 3070.029 Million cell updates/sec
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AX44046 Sequence

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AX464040 Sequence

AC025574 Homo sapi

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AC109891 Rattus no

AF186113 Homo sapi

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Eukaryota; Metazoa; C
Mammalia; Eutheria; I
1 (bases 1 to 798)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Der
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
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Guntratne, P.H., García, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (22-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC008261.1 GI:14198400
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                                                                                                                                                                                                             /translation="mkGwGwLallLGvLLGTawarrsQDLHCGaCralvDeleweiar
VDPKKTIQWcSeriwPDGsQGSVVEVPYARSEAHLTELLEEVCDRWKEYGEQIDPSTHR
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                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV-SPORT6"
115. .663
                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Mammary tumor.months old, gross tissue."
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                                                                                                                                                                                                     DKLCSKRTDLCDHALHRSHDEL
                                                                                                                                                                                                                                                                        /product="transmembrane protein
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/db_xref="GI:14198401"
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                                                                                                                              /db_xref="LocusID:56530"
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                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                     2 (bases 1 to 1017)
Sheppard, P., Jelinek, L.,
                                                                                                                                                                                                                                                                    Mus musculus putative secreted Unpublished
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Sheppard, P., Jelinek, L.,
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Mammalia; Eutheria;
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                                                                                                                                                        Location/Qualifiers
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                                                                                                                           organism-"Mus musculus"
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(Zsig9) mRNA, complete
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                                                                        Homo sapiens chromosome 12 clone SEQUENCE, 5 unordered pieces. AC012013
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 158198)
                                                        HTG;
                                              Homo
                                                              AC012013.18 GI:14717292
                                     Homo
                                  sapiens
                                                 HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                          sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         */Translation="MKGWGWLALLLGVLLGTAWARRSQDLHCGACRALVDELEWEIAR VDPKKTIQMGSFRINPDGSQSVVEVPYARSEAHLTELLEEVCDRMKEYGEQIDPSTHR KNYVRVVSRNGESSELDLGGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK DKLCSKTDLCDHALHRSHDEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative secreted protein ZSIG9"
/protein_id="AAF01433.1"
/db_xref="GI:6014636"
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Benton, J., Blange, K., Blankeburg, K., Bennin, D., Bouck, J., Benten, J., Charles, J., Chavez, D., Chen, G., Chen, R., Chen, C., Chen, G., Chen, R., Chen, J., Charles, J., Chavez, D., Chen, G., Chen, R., Chen, J., Chen, J.,
Worley, K.C
                                                                                                                                                Direct Submission
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                                                   (bases 1 to 158198)
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Banks, T., Barbaria, J.,
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COMMENT

Direct Submission

TITLE JOURNAL

Submitted (19-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2001 this sequence version replaced g1:14547727.

Genome Center

Center: Baylor College of Medicine Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: Project Information

밁 Ş 밁 Ş

Center project Information
Center project name: HMKZ
Center clone name: RP11-764L14
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 16127% bases at least 040
Consensus quality: 174843 bases at least 020
Estimated insert size: 1638803; sum-of-contigs estimation
Quality coverage: 6x in 020 bases; agarose-fp estimation
Quality coverage: 5.8x in 020 bases; sum-of-contigs estimation sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                             ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
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8230 108329: gap of unknown length
8330 150246: contig of 41917 bp in length
0247 150346: gap of unknown length
0347 153410: contig of 3064 bp in length
3411 155310: gap of unknown length
3511 15539: gap of unknown length
3511 15539: gap of unknown length
5740 158198: contig of 2229 bp in length
5840 158198: contig of 2359 bp in length
5840 158198: contig of 3359 bp in length
5840 158198: contig of 359 bp in length
5840 158198: contig of 359 bp in length
5840 158198

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-764L14"

7 a 30922 c 31747 g 49030 t 442 others
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CORIXA CORPORATION (US)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Lodes,M.J., Algate,P.A., Fling,S.
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/db_xref="taxon:9606"
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Catarrhini; Hominidae;
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                               GAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-JUN-1998) Soishi Kato, Research Institute of I Rehabilitation Center for the Disabled, Department of Rehabilitation Engineering: 4-1 Namiki, Tokorozawa, Saitama 359-855, Japan (E-mail:seeishierabb.go.) Tel:042-995-3100(ex.2568), Fax:042-995-3132)
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Homo sapiens gastric adenocarcinoma cDNA clone_lib:pKAl-meta-1 clone:HP10390.

Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/protein_1d="BAA76498.1"
/protein_1d="BAA76498.1"
/db_xref="GI:4586840"
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/translation="MKG86WLALLLGALLGTAWARRSODLHCGACRALVDELEWEIAQ
/TPKKTTOMGSERINDDOSQSVVEVPYARSEAHLTELLEEICDRMKEYGEQIDPSTHR
KNYVRVVGRNGESSELDLQGIRDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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/clone_lib="pKA1-meta-1"
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                                                                                                                                                                                                                                                              Submitted (13-APR-2001) Neuroscience,
Husargatan 3, Uppsala 75123, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           Bornhauser, B.C., Olsson, P.-A. NSAP is a novel saposin-like pstimulates neurite outgrowth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens saposin-like protein mRNA, AY032624
AY032624.1 GI:20196198
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Olsson, P.-A. and Lindholm, D.
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/translation="MKGWGWLALLLGALLGTAWARRSODLHCGACRALVDELEWEIAQ VDPKKTIQMGSERINPDGSQSVVEVPYARSEAHLTELLEEICDRMKEYGBOIDPSTHR KNYVRVVGRNGESSELDLQGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK DKLCSKRTDLCDHALHISHDEL"

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269 c 343 g 230 t
                                                                                                                                    /note="NSAP; encodes a type 2 membrane
putative ER retention motif"
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/protein_id="AAK38148.1"
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AX464040
                                                                                                                                                                Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
                                                                                                          Genentech
                                                                                                                      Patent:
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                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                             Location/Qualifiers
                                                                                                                                          and transmembrane polypeptides
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                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
316 c 379 g 25
                                                                                                                                                         and Zhang, Z.
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Primates;
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Length:
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Percent Similarity:
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     Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Blange, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunky, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Davida, M.L., Davis, C., Davy-Carroll, L., Daderich, D.A., Davida, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Daper, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Daper, H., Dugan-Rocha, S., Durbin, K.J.,
                                                                                                                                                                                                                            AC025574
Homo sapiens chromosome 12 clt
SEQUENCE, 12 unordered pieces
AC025574
                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                             Homo sapiens
                                                                                                                                         Mammalia; Eutheria; Pr
1 (bases 1 to 155023)
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98.35%
97.25%
97.81%
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ASE1; HTGS_DRAFT
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le 12 clone
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Conservative:
Mismatches:
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Harris,C., Harris,K., Harlaw, Havis,A., name,D., name, Harris,C., Harris,K., Hart,M., Havisk,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Jacobson,B., Homasi,F., Humer,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kursshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H., Massey,E., Mahashari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Massey,E., Mawhiney,E., McLeod,M.P., Maedor,M., Mei,G., Metzker,M., Moser,M., Neel,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,J., Pickens,R., Primus,E., Pu,L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojlbokan,I., Rolfe,M., Ruiz,S., Savery,G., Sodergren,B., Sonaike,T., Shooshtari,N., Sisson,I., Sodergren,B., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sumani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wallsiamson,A., Walczyk,R., Wooden,S., Ward-Moore,S., Warren,R., Washington,S., Wallsiandon,A., Wileczyk,R., Wooden,S., Watlianson,S., Wallsiandon,S., Wallsiandon,S., Mu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Wallsiandon,S., Wallsiandon,S., Mallsiandon,A., Wileczyk,R., Wooden,S., Watlialon,S., Mallsiandon,S., Mallsiandon,S., Nelson,D., Weinstock,G. and Glbbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 3, 2002 this sequence version replaced g1:20335511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Direct Submission
Direct Submission
Submitted (11-MAR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                           NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                               Center clone name: RP11-348M3

Sequencing vector: M.3;
Chemistry: Dye-primer Bodipy: 5% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 141522 bases at least Q40
Consensus quality: 147097 bases at least Q20
Estimated insert size: 150706; sum-of-contigs estimation
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GACAATGTTAAAAGACAAACTTTGCAGTAAGCGAACAGGTAAGCTGCCCCCACTTTATCTC 55641
                                   ASPASnValLysAspLysLeuCysSerLysArgThr-----
                                                                                                                             CysGluSerIleValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAla 156
                                                                                                                                                                                          AAGTGAAGGCAAGAGGCCTCTTATTGCCCCTGTGTCACCCATTTCTCCCCTTGGGTTGGCAG 55761
                                                                                                TGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                   MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgVal 108
                                                                                                                                                                                                                                                                                                                                                                                 ATTAGCGGCACCCTCAAGTTTGCGGTGAGCTATGGGAATCGGTAGCTGGTTCTTGGACAT 55881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGAT 55941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24750; gap of unknown length
31778: contig of 7028 bp in length
31878: gap of unknown length
42263: contig of 10385 bp in length
42363: gap of unknown length
5104: contig of 8741 bp in length
51204: gap of unknown length
51204: gap of unknown length
68306: contig of 17102 bp in length
68306: contig of 17102 bp in length
109481: contig of 41075 bp in length
109481: contig of 41075 bp in length
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3: contig of 45442 bp
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REFERENCE AUTHORS TITLE

Worley, K.C.

Submission

JOURNAL

Contact: hgsc-help@bcm.tmc.edu Web site: http://www.hgsc.bcm.tmc.edu/ Center: Baylor College of Medicine Center code: BCM

Center project name: HALV

3033: contig of 3033 bp in length

TITLE
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AUTHORS
TITLE

Worley, K.C. Unpublished

(bases 1 to 155023)

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AC073896/c
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Allen, C., Adians, C., Adio-Oduola, B., All-osman, F.R., Allen, C., Alsbrooks, S.L., Ameratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Blimage, K., Blankenburg, K., Bonnin, D., Buck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Boron, M., Bryant, N.P., Bouck, J., Chacko, J., Chac
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Homo sapiens chromosome 12 clone RP11-977G19, WORKING DRAFT
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatck, A., Tabbor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S. Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Ward, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length
                           46453
                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-primer Bodipy: 15% of reads (Chemistry: Dye-terminator Big Dye: 85% of reads Assembly program: Phrap; version 0.990329 (Consensus quality: 179279 bases at least Q40 (Consensus quality: 180581 bases at least Q30 (Consensus quality: 180731 bases at least Q20 (Consensus quality: 181073 bases at least Q20 (Consensus quality: 181073 bases at least Q20 (Consensus Quality: 181073 bases; sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 182350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: HBWI center clone name: RP11-977G19 ---- Summary Statistics sequencing vector: Plasmid; Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                     2894
2994
6687
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                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                 /clone="RP11-977G19"
                                                                         /chromosome="12"
                                                                                                                                                                                                          85994: gap of unknown 182350: contig of 96356
                                                                                                                                                                                                                                                                              2893: contig of 2893 bp in length 2993: gap of unknown length 6686: contig of 3693 bp in length 6786: gap of unknown length 17251: contig of 10465 bp in length 17351: gap of unknown length 67864 gap of unknown length
                                                                                                                                                                                                                                                              85894: contig of 68543 bp in
                                                                                                                                                                                    'Qualifiers
                     43855 g
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Mammalla: Eutherla: Primates; Catarrhini; Hominidae; Homo.

Mammalla: Eutherla: Primates; Catarrhini; Hominidae; Homo.

BE 1 (bases 1 to 184762)

BE 1 (bases 1 to 184762)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,

Barbarla,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,

Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,

Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,

Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Earnhart,C., Edgar,D., Edwards,C., Elhaj,C., Escotto,M.,

Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,

Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,

Garrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,

Harris,C., Hart,M., Hallak,P., Hawes,A., Hernandez,J.,

Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,

Jacobson, B., Jia,Y., Johnson, R., Jolivet, S., Hume,J., Jackson,L.E.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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sapiens chromosome 12 clone RP11-183H16,
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Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, S., Oguh, M., Morgan, M., Morris, S., Miller, N., Okwonu, G., Oragunye, N., Oldedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pilkens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, J., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Walldamson, A., Walczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R.
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On A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Center project Information
Center project name: HAPC
Center clone name: RP11-183H16
Center clone name: RP11-183H16
Sequencing vector: Plasmid;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 183845 bases at least Q40
Consensus quality: 184849 bases at least Q30
Consensus quality: 185447 bases at least Q30
Estimated insert size: 159026; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C.
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Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
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* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

as soon as it is available and the accession number will be preserved.

contig gap of

of 2040 bp in length

2041 2141 4171

4170: 4270: 2040:

contig of 2030 r gap of unknown l contig of 4024 l

bp in length

length

unknown of 2030

bp in length length length

AUTHORS TITLE JOURNAL

JOURNAL

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                                                                                                                                     AspasnValLysAspLysLeuCysSerLysArgThr 168
                                                                                                                                                                               CysGluSerIleValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAla 156
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                                                                                                                                                                                                                                                                                                                                       IleSerGlyThrLeuLysPheAla------
                                               sequence.
AC090489
AC090489.8
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                 AC090489
Genomic sequence
                             Mus musculus.
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1..184762
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-183H16"
a 44751 c 45101 g 46673
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si gap of unknown length

si contig of 18780 bp in 1

si gap of unknown length

si contig of 19119 bp in 1

si gap of unknown length

si contig of 31790 bp in 1

si gap of unknown length

scontig of 35738 bp in 1

si gap of unknown length

si gap of unknown length

si gap of unknown length

scontig of 64639 bp in 1
                                                                                 207424 bp
Mus musculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
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                                                                                 DNA linear Roclone RP23-104010,
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GGAGTTATAGGGATTCCCTGGCACAGGATGGGAGATGGGATGCGGAAGTGGTTTGCCTAC
                                                                        ATCAGCGGCACCCTCAAGTTTGCGGTGAGTTACCGCTGTGCCGTGAGTAGCTGTTTCTTG
                                                                                                                                                                                                                           on Jan 26, 2002 this sequence version replaced gi:18201765. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-JAN-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-FEB-2001) Lita Annenberg Center, Cold Spring Harbor Laboratory, Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCombie,W.R., de la Bastide,M., Spiegel,L., Preston,R.,
Kirchoff,K., Kuit,K., Nascimento,L., Zutavern,T., Ballja,
Bell,M., Baker,J., Santos,L., Miller,B., Katzenberger,F.,
Bell, K., King,L., Yang,C., Palmer,L., O'Shaughnessy,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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/db_xref="taxon:10090"
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is a mononuclectide (T) repeat in which the
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                                         Barbaria, J., Benton, J., Binage, K., Are, J.R., Ayele, M., Banks, T., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burch, E., Brown, M., Bryant, N.P., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H. H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Gae, J., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiser, M., Massey, E., Mawilney, E., McLeod, M.P., Meador, M., McLer, E., Martin, R., Wartinda, A., Norgan, M., Morrin, S., Massey, E., Mawilney, E., McLeod, M.P., Meador, M., McLer, E., Nockens, R., Plimus, E., Puthers, L., Pickers, R., Primus, E., Put, L., Ollies, M., Okwionu, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stanley, H., Stanley, 
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Eukaryota; Metazoa;
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Rodentia;
                       Shen, H., Shooshtari, N., Si, T., Sparks, A., Stanley, H.,
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     Tamerisa, A.,
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Tang, H.
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Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced of:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                           Jul 12, 2002 this sequence version replaced gi:18860222.
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 60229 bases at least Q40
Consensus quality: 63959 bases at least Q30
Consensus quality: 66730 bases at least Q20
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Center clone name: CH230-319E6
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14201 15841 15941 17054 17154 12363 12463 14101 8141 10044 10144 10138 11238 1424 1524 2973 3073 4718 12362: 12462: 14100: 1423: contig of 1423 bp in length 1523: gap of unknown length 2972: contig of 1449 bp in length gap of unknown contig of 1645 gap of unknown contig of 1815 gap of unknown contig of 1308 gap of unknown gap of unknown contig of unknown gap unknown gap of unknown gap unknown gap of un gap of gap of contig gap of contig gap of contig gap gap of contig contig gap of contig 9 of 1640
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AUTHORS TITLE . JOURNAL EFFERENCE AUTHORS TITLE	AF186113 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	136 98052 (150 (98112)	20 5	ω ω Ν υ	20 5	135 97812 (29 52	109 ·	97632	69 97572	
I (bases 1 to 649) Sheppard,P., Jelinek,L., Whitmore,T., Blumberg,H., Lehner,J. and O'Hara,P. Homo sapiens putative secreted protein Unpublished 2 (bases 1 to 649) Sheppard,P., Jelinek,L., Whitmore,T., Blumberg,H., Lehner,J. and O'Hara,P. Direct Submission	AF186113 649 bp mRNA linear PRI 13-JAN-2000 Cds. AF186113 AF186113 AF186113 AF186113 AF186113 AF1861131 GI:6014631 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		AAACCAGGGAGAGAGCTGAGCCGGTGTCTCTGCCCCGGCTGAGGATCCTGGGTCACTTCT 98051	TCTAGGCCAGCTGGAGCGATATCATAAAACCCCTGTCTATAAAATCCCCAACTGCCACCCAA 97991	CTTGTAACCCGGGCAGTGGAGGAGCAGTGGTTGGAAGATTGGCACTAGTTCATACTGAGT 97931	GGAGTTCATAGGGATTCCTGGGCACAGATTGGGAGTCGGCGGCGGATATGGTGTTGCATG 97871	IleSerGlyThrLeuLysPhe	ValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp 128 	MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgVal 108 	alProTyrAlaArgSerGluAlaHisLeuThrGl TTCCTTATGCCCGCTCAGAGGCCCACCTCACGGA	IN Innent Scores: 7.06e-32

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                                                                                                                                                                                                                                                                                                                                   GATGGCAGCCAGTCAGTGGTGGAGGTA 310
                                                                     Direct Submission
Submitted (17-NOV-2000) National Institutes of Health, Mammalian Submitted (17-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin
                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                       Strausberg, R.
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 824)
                                                                                                                                                                                                                               BC001027.1
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                                                                                                                                                                                                                                                      IMAGE: 3344788, mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-SEP-1999) Biomolecular Informatics, ZymoGenetics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175
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RESULT 15
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                                                                                                                                                                                                                                        GlulleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro 60
                   Rattus norvegicus clone CH230-208H17, *
***, 42 unordered pieces.
AC103156
AC103156
AC103156.3 GI:21731105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: p Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6014631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: nisc_mgc@nhgri.nlh.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.
Bietrich,N.L., Guan,X., Gupte,J., Ho,S.-L., Karlins,E., Legaspi,R.
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
The Array Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center (NISC),
Gaithersburg, Maryland;
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Legaspi, R.,
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HTGS_PHASE1.

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced g1:17974643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 69753)
Worley,K.C.
Direct Submission
Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 69753)
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Rattus norvegicus
Eukaryota; Metazoa;
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                             Center: Baylor College of Medicine
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Rodentia;
or Big Dye:
; version 0.
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Consensus quality: 15506 bases at least Q40
Consensus quality: 17125 bases at least Q30
Consensus quality: 18271 bases at least Q20
Consensus quality: 18271 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 42 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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39477 39577 41222 41322 41323 43131 37672 37772 35868 35968 34616 34716 28430 30047 30147 31614 31714 33121 33221 25396 25496 26516 26516 26616 28330 5270 6914 6914 6918 6918 8120 9385 9485 10997 110997 112555 112655 114377 114477 11477 115791 22640 23862 23962 18408: 19786: 18308: dab of i conti gap of conti gap gap of gap o gap o gap o contig gap of conti gap of contic gap of gap of gap o gap of contig gap of contig gap o gap o gap of contig contig conti contig gap of contig of 1645 unknown of 1809 y of 1722
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Search completed: March 31, 2003, 03:39:46 Job time : 1885.3 secs	OY 52 GlnMetGlySerPheArgIleAsnProAspGlySerGlnSerValValGluValProTyr 71	32 ATGALBLEUVALASPGLULEUGLUTTPGLUILEALBATGVBLASPPTOLYSLYSTHTILE 51	Alacys 31 14948 TTGGGTTGACCCATCCCCTCACGATCCCCCACTCCCTATTCTCTTCCTGGCGCCAGCTTGC 14	10 100 GGAAGCCGACCCTTGGGAGTCATTAG	29	21 ArgArgSerGlnAspLeuHisCysGly2	1 MetLysGlyTrpGlyTrpLeuAlaLeuLeuGlyValLeuLeuGlyThrAlaTrpAla 2	US-10-082-502-19 (1-182) x AC103156 (1-69753)	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Percent Similarity: S7.50% Best Local Similarity: Ouery Match: 35.09% DB: Alignment: Conservative: Mismatches: Gaps: 1	17500 a 17000 C 1/39	/drganism="kattus norvegicus" /db_xref="taxon:10116" /clone="CH230-208H17"	on/Qualifiers	* 67754 69753: contig	67654 67753: contig of 2669 bp in	64885 64984: gap of unknown len	2710 62809: gap of unknown length	60622 60721: gap of unknown length	59104 59103: gap of unknown length 59104 60621: contig of 1518 bp in le	57597 59003: contig of 1407 k	54742 57496: contig of 2755 bp 1	53168 54641: contig of 1474 bp in 54642 54741: gap of unknown length	1160 53067: contig of 1908 b 3068 53167: gap of unknown 1	51060 51159: gap of unknown	49062 49161: gap of unknown length	46200 46299: gap of unknown length 46300 49061: contig of 2762 bp in length	44835 46199: contig of 1365	11775 11071 25 26
	71 14769		31 14889	14949	29	29 15009	20 15069																				

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Command line parameters:

MODEL-frame+_p2n.model -DEV=xlp

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1

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RESULT 2
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AX440456
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Compositions and methods for the the
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                                                                                                                                                                                                   GluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGG
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Homo sapiens gastric adenocarcinoma
Clone_lib:pKAl-meta-1 clone:HP10390
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Homo sapiens mRNA for type II
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/protein_1d="BAA76498.1"
/protein_1d="BAA76498.1"
/db_xref=="G114586840"
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/translation="MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQ
/TRANSLATIOMGSFRINPDGSQSYVEVPYARSEAHLTELLEEICDRWKEYGEQIDPSTHR
KNYVRVYGRWGESSELLDGGIRGDESTLKFACESIVEEYEDELIEFFSREADNVK
DKLCSKRTDLCDHALHISHDEL"
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/db_xref="taxon:9606"
/clone="HP10390"
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/clone_lib="pKA1-meta-1"
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269 c 343 g 230 t
                                                                                                                                                                                                                                                                                                                                   /note="NSAP; encodes a type
putative ER retention motif"
                                                                                                                                                                                                                                                                                   /product="saposin-like protein"
/protein_id="AAK38148.1"
/db_xref="GI:20196199"
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/chromosome="12"
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{\tt GluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro}
                      ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
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Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
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Sequence 173 from Patent
AX464040
AX464040.1 GI:21899037
                                                                                                                                                                                                                                                      Genentech
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                                                                                                                                                                                                                                                                              Secreted and transmembrane polypeptides and nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                   USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Der
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
                                                  Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov/Series: IRAK Plate: 5 Row: b Column: 23
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (22-MAY-2001) National Institutes of Health, Mammalian Submitted (26-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Guntaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
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IMAGE:2650612, mRNA, co:
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BC008261.1 GI:14198400
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                                      lone was selected for full length sequencing because it the following selection criteria: matched mRNA g1: 9903606
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  /organism="Mus musculus"
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Mus musculus
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KNYVRVVSRNGESSELDIGGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
DKLCSKRTDLCDHALHRSHDEL"
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                         GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-SEP-1999) Biomolecular Informatics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus putative secreted protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sheppard, P., Jelinek, L., Whitmore, T., Blumberg, H., Lehner, J. and
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/protein_id="AAF01433.1"
/db_xref="G1:6014636"
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1. .1017
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/db_xref="taxon:10090"
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Submitted (19-0CT-1999) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2001 this sequence version replaced gi:14547727.
                                                           Direct Submission
                                                                    Worley, K.C.
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RES MUZNYD, M., Addins, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N., Buck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N., Buck, J., Buck, J., Buck, J., Burkett, C., Burrell, K.L., Byrd, N.C., Carren, T.F., Buhay, C., Carren, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, J., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunardne, P., Hale, S., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Joudah, S., Karlsson, E., Kellys, S., Khan, U., King, L., Korvah, J., Kureshi, A., Landry, M., Leal, B., Lewis, L., Li, J., Li, K., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Mapua, P., Martin, R., Martindale, A., Mapus, R., Ketzker, M., Mapua, P., Martin, R., Martindale, A., Morgan, M., Mortis, S., Noser, M., Neal, D., Newtson, J., Newtson,
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Homo sapiens chromosome 12 cl
SEQUENCE, 5 unordered pieces.
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152351 TTGCTTGAGGAGGTGTGTGACCGAATGAAGGAGTACGGGGAACAGATTGACCCTTCTACC
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NOTE: This is a "vorking draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 161278 bases at least Q30
Consensus quality: 170806 bases at least Q30
Consensus quality: 174843 bases at least Q20
Consensus quality: 174843 bases at least Q20
Estimated insert size: 168803; sum-of-contigs estimation
Ouality coverage: 6x in Q20 bases; sqarose-fp estimation
Quality coverage: 5.8x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
------Project Information
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1230 108329: gap of unknown length
1230 150246: contig of 41917 bp in length
1247 150346: gap of unknown length
1247 153410: contig of 3064 bp in length
1341 153510: gap of unknown length
1511 155739: contig of 2229 bp in length
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1540 156198: contig of 2359 bp in length
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Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Ara, J.R., Ayele, M., Banks, T.,

Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (09-MAY-2002) Human Genome Sequencing Center, Depail of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On May 3, 2002 this sequence version replaced gi:20335511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 155023)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Chemistry: Dye-primer Bodipy: 5% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 141522 bases at least Q40
Consensus quality: 147097 bases at least Q20
Consensus quality: 150442 bases at least Q20
Estimated insert size: 150706; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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BASE COUNT ORIGIN Query Match: US-10-082-502-20 (1-162) x AC025574 (1-155023) Best Local Similarity: Pred. No.: Alignment Scores Percent Similarity: Score: 49 ValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluIleCysAspArg 56000 55340 55400 55460 55580 55700 55760 55820 AAGTGAAGGCAAGAGGCCTCTTATTGCCCTGTGTCACCCATTTCTCCCTTGGGTTGGCAG 55761 55880 55940 55520 55640 156 HisIleSerHisAspGluLeu 162 148 148 148 116 109 137 117 116 89 69 TGAGAATGGCATATTCCTTTAAATTGTTTTGCCATTTGCAGATCTTTGTGACCATGCCCTG ValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp 108 MetLysGluTyrGlyGluGlnIleAspProSerThrH1sArgLysAsnTyrValArgVal TGGTGTGTGTTGTGTCAGCTTGGTCTGGGAAATTTTCTTGATACTGGCAGATATCAGTA 55341 GGTGAGAGGACAGTGGGGATGTTTTATCATTTATAAGCATATATTCTGCAGAATGGTGGT 55401 GAAACCTCTGGTATTAGGTCAAGAGCTGTCTTCCATTTCCCTTGGCTTAGGGGACTTGGG 55521 CTGTTCTAGTAGCTCTGTGGAACCTGACATTCCCTAACTCACCCCATACACCCCCCATCCCA 55581 GACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAGGTAAGCTGCCCCCACTTTATCTC 55641 TAAGGGGTTGTTGGAGAACCAATTAGAAAGTTAGGCTGATATCCTTGTCCTCCTCTTTGG GTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGAT GTGTTCCTCCACATTTTCTGTCAGCTTTCAGAATTTGTGTCCCCTTGACCCTGAGATACA 55461 ATTAGCGGCACCCTCAAGTTTGCGGTGAGCTATGGGAATCGGTAGCTGGTTCTTGGACAT 55881 40008 a 36207 488.50 39.72% 39.72% 39.72% 57.61% 7.01e-38 ი 35987 φ ------AspLeuCysAspHisAlaLeu 155 Matches: Conservative: Mismatches: Indels: Gaps: 41693 rt 1128 others 155023 114 0 0 173 148 116 116 116 148 148 56001 88 55281 148 148 148 55821 55941 56061 83

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RS MIZNY,D.M., Addams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Ara,J.R., Ayele,M., Banks,T., Barbarla,J., Benton,J., Binage, H.C., Ara,J.R., Ayele,M., Banks,T., Barbarla,J., Bowle,S., Bireva,M., Brown,E., Brown,M., Bryant,N.P., Buck,J., Bouck,J., Burch,P., Burkett,C., Burch,P., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burch,L.K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Davila,M., J., Christopoulos,C., Escotto,M., Earnbart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Earnbart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Earnbart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Ganez,T., Garza,N., Gill,R., Gorrell,J.T., Govara,W., Gunaratne,P., Halles,S., Hamilton,K., Hernandez,J., Homard,S.C., Hartis,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,D., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Hernandez,D., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Jac,Son,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kally,S., Khan,U., King,L., Korsh,J., Koyar,C., Kratovic,J., Kureshi,A., Landry,N., Laudey,M., Loulseged,H., Li,J., Lichtarge,O., Lieu,C., Liu,J., Liu,M., Loulseged,H., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Karlsson,E., Martina,R., Martindale,A., Martinez,E., Mansay,E., Martina,R., Martindale,A., Martinez,E., Mansay,E., Martina,R., Martindale,A., Martinez,E., Massay,E., Martina,R., Martindale,A., Martinez,E., Martina,R., Martindale,A., Martinez,E., Martina,R., Martindale,A., Martinez,E., Martina,R., Martindale,A., Martinez,G., Welker,M., Molloway,R., Stone,H., Stone,H., Shooshtari,N., Sisson,I., Ford,R., Martin
                                                                                                                                                 Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 23, 2002 this sequence version replaced gi:22296903.
                                                                                                                                                                                                                                                                                                                                                         Submitted (01-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 182350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182350 bp DNA linear HTG 24-, HOMO sapiens chromosome 12 clone RP11-977G19, WORKING DRAFT SEQUENCE, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                       Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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1 (bases 1 to 182350)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases
                                                            Center: Baylor College of Medicine Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTGS_PHASE1;
                                                                                                                                                                                                                                                                                               Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 to 182350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa; Chordata;
Eutheria; Primates;
                                                                                                                      Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 24-AUG-2002
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Db 171787 TAAGGGGTTGTTGGAGAACCAATTAGAAAGTTAGGCTGATATCCTTGTCCTCCTCTTTGG 171728
                                                                                                                                                                                                                                                                                                                                                             Db 171907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 172027 GTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-082-502-20 (1-162) x AC073896 (1-182350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171967
                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 ValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluIleCysAspArg
                                                                                                                                                                                                                                                                                                                                                                                                  89 ValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp 108
                                                                                                                                                                                                                        GTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGAT 171848
                                                                                                                                                                     ATTAGCGGCACCCTCAAGTTTGCGGTGAGCTATGGGAATCGGTAGCTGGTTCTTGGACAT 171788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-primer Bodipy: 15% of reads Chemistry: Dye-terminator Big Dye: 85% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 179279 bases at least 040 Consensus quality: 180581 bases at least 020 Consensus quality: 180581 bases at least 020 Consensus quality: 181073 bases at least 020 Consensus quality: 180581 bases 020 Consensus quality: 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid; Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: RP11-977G19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: HBWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2894
2994
6687
6787
17252
17352
85895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location,
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481.00
63.80%
63.19%
56.72%
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2993: gap of unknown length
6686: contig of 3693 bp in length
6786: gap of unknown length
17251: contig of 10465 bp in length
17351: gap of unknown length
85894: contig of 68543 bp in length
85994: gap of unknown length
182350: contig of 96356 bp in length.
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 others
                                                                                                                                                                                                                                                            116
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Db 171547 CTGTTCT 171541
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                                                                                                                                                                         Barbarla, J. Blande, K. Blankenburg, K., Banks, Y.,
Barbarla, J. Benton, J. Blange, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowle, S., Brevan, K., Brown, E., Brown, M., Bryant, N. P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R.,
Davila, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A.,
Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H.,
Douthwalte, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Herria, C., Hartis, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Homsi, F., Howard, S., Hatt, M., Havlak, P., Hame, J., Jackson, L. E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Morgan, M., Morris, S.,
Noser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Origunye, N., Oriedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L. J., Ollies, M., Ren, Y.,
Sodergren, E., Sonatke, T., Sparks, A., Stanley, H., Stone, H.,
Sodergren, E., Sonatke, T., Sparks, A., Stanley, H.,
Mang, S., Ward, Morse, S., Warren, R., Washington, C., Watlingon, S.,
Wu, Y., Wu, Y. F., Zhou, J., Zortilla, S., Nelson, D.,
Wang, S., Wang, O.,
Walliamson, A., Wleez, S., Washington, C., Watlington, S.,
Wu, C., Wu, Y. F., Zhou, J., Zortilla, S., Nelson, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAGGTAAGCTGCCCCCACTTTATCTC 171548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CysGluSerIleValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAla 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspAsnValLysAspLysLeuCysSerLysArgThrAsp-LeuCysAspHisAlaLeuHi 156
                                                                                                                                   Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC023500 184762 bp DNA linear HTG 24-, HOMO Saplens chromosome 12 clone RP11-183H16, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC023500.32 GI:22095070
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC023500
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                              (bases 1 to 184762)
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Primates;
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Direct Submission

Submitted (15-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baylor Plaza, Houston, 'IX //טיטי, טיסה On Aug 4, 2002 this sequence version replaced g1:22094227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator Blg Dye: 98% of reads
Chemistry: Dye-terminator Blg Dye: 98% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 183845 bases at least Q40
Consensus quality: 184449 bases at least Q30
Consensus quality: 185447 bases at least Q30
Consensus quality: 185447 bases at least Q30
Consensus quality: 185487 bases at least Q30
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Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
Project Information
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/db_xref="taxon:9606"
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4170: contig of 2030 bp in length
4270: gap of unknown length
8294: contig of 4024 bp in length
8394: gap of unknown length
84196: contig of 5802 bp in length
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6: contig of 18780 bp in length
5: contig of 19119 bp in length
5: gap of unknown length
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REFERENCE AUTHORS

SOURCE ORGANISM

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                                                                                                                                                                                                                                                                                                                                                                                                              AspAsnValLysAspLysLeuCysSerLysArgThrAsp-LeuCysAspHisAlaLeuHi 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAGGGGTTGTTGGAGAACCAATTAGAAAGTTAGGCTGATATCCTTGTCCTCCTCTTTGG 43785
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                                Center, Cold Spring Harbor
Harbor, NY 11724, USA
3 (bases 1 to 207424)
                                                                                                                                                                                      Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 207424)
                                                    Submitted (24-FEB-2001) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor Laboratory, 1
 Submitted (26-JAN-2002) Lita
                        McCombie, W.R
                                                                                                            Unpublished
                                                                                                                         sequence
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Genomic sequence
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                                                                                          McCombie, W.R.
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for Mus musculus,
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Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
On Jan 26, 2002 this sequence version replaced gi:18201765.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
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Source 1.207424
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MetlysclutyrglycluglnileaspproserthrHisarglysasnTyrvalargval 88

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                                                                                       Worley K.C.

Morley K.C.

Direct Submission
Submitted (08-FEB-2002) Human Genome
Submitted (08-FEB-2002) Human Genetics, Bayl
Amuston, TX 77030, USA
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                     Unpublished 2 (bases 1
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                                                          Direct Submission
                                                                         Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M.,
                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1.
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                                                                                                                          Sequencing Center, Depa
lor College of Medicine,
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                                                                                                                                         Department
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft'

* CONSISTS of 47 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990339 Consensus quality: 60229 bases at least Q40 Consensus quality: 63959 bases at least Q30 Consensus quality: 63730 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: Plasmid;
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Center clone name: CH230-319E6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTCTTCTTGGTCGGCAGTGTGAGAGCATTGTGGAGGAGTACGAGGATGAACTTATTGA
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                                                                                                                                                                                                                                                   Submitted (14-SEP-1999) Biomolecular Informatics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 649)
Sheppard,P., Jelinek,L., Whitmore,T., Blumberg,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 649)
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                                                                                                                                                                                                                                                                                                                                                        Homo sapiens putative 
Unpublished
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/product="putative secreted protein ZSIG9"
|protein_id="AAF01431.1"
|protein_id="AAF01431.1"
|/db_xref="GI:6014632"
|/translation="MMGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQ
|/translation="MMGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQ
VDPKKTIQMGSFRINPDGSQSVYEVTVTVPPNKVAHSGFG"
                                                                      /gene="ZSIG9"
/codon_start=1
                                                                                                     /gene-"ZSIG9"
104. .358
                                                                                                                                                               /db_xref="taxon:9606"
/chromosome="12"
/map="12q15"
                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="dbEST:R15306"
                                                                                                                                                 /clone="IMAGE: 29675"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/ILNL at: http://lmage.llnl.gov series: IRAL Plate: 5 Row: p Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6014631.
                                                                                                                                                                                                                                                                             Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,Q.L., Masitello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortiu DNA Sequencing by: National Institutes of Health Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (17-NOY-2000) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg,R
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Mammalia; Eutheria;
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                                 /organism="Homo sapiens"
/db_xref="LocusID:10330"
/db_xref="taxon:9606"
                                                                                                                         Cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                     NEDO human cDNA sequencing project Unpublished
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Homo sapiens cerebellum cDNA to mRNA, clone_lib:BRACE2
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2378 bp mRNA linear
Homo sapiens cDNA FLJ37126 fis, clone BRACE2022693,
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Eutheria; Primates;
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194 c 233 g 176 t
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full insert sequencing:
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PRI 15-JUL-2002 weakly similar

Isono, Y.,

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Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: March 31, 2003, 03:42:06 Job time: 1675.7 secs
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379
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                                                                                                                                                                                                                                      200 AAGGAGAACTTTCAAGAGATTCGCTCCTAGGAAAGGAGACAAAATATACCAAGAATTT 259
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlp
-O-/cgn2_1/USPTO_spool/VGS1082502/runat_24032003_135100_6599/app_query.fasta_1.1308
-DB-EST -OFMT-fastap -SUFFIX-rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DCCALICK-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-UNITSTO -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US10082502_eCGN_1_1_5425_e_unat_24032003_135100_6599 -NCDP-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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                                        em_gss_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 BM832828

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE DEFINITION AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 588)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R. Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and 588 5', mRNA sequence. BM832828 BM822828.1 GI:19189237 EST. Homo sapiens numan. , Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and bp mRNA linear EST 06-MAR-2002 sapiens cDNA clone S5SNU48491-11-B03

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                                                                                                                     21 GluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro 40
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GAAATTGCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCA
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21C Frontier Korean E
Unpublished (2002)
Contact: Kim YS
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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Plate: 11 row: B column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was decapped with tabacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof' by electroporation method. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5 primer and N(CT)14 as 3 primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Toplof' with electroporation method."
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FEATURES
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1 (bases 1 to 591)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: yongsung@mail.kribb.re.kr
Plate: 11 row: H column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Kim YS
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21C Frontier Korean
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BM832888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop:
/note-*Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was decapped with tabacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method.
                                                                                                                                                                                                                    /tissue_type="Stomach"
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/cell_line="SNU-484"
                                                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"S5SNU484s1-11-H01"
                                                                                                                                                                                                /lab_host="Top10F'"
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                                                                                                                                                                                                                                                                                               /clone_lib="S5SNU484s1"
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1 ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
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                                                                                                                    1 bp mRNA linear Egsapiens cDNA clone IMAGE:50
TYPE II MEMBRANE PROTEIN.
                                                                                                                                      linear EST 11-MAR-2002
ne IMAGE:5085832 5'
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HisArgLysAsnTyrValArgValValGlyArgAsnGlyGluSerSerGluLeuAspLeu
                                                                                                                  GATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAG
                                                                                                                                      AspGlySerGlnServalValGluValProTyrAlaArgSerGluAlaHisLeuThrGlu
                                                                                                                                                                                              GAAATTGCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCA
                                                                                                                                                                                                               GlulleAlaGlnValAspProLysLysThrIleGlnMetGlySarPheArgIleAsnPro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
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MA 02138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Ir
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endocrine Pancreas Consortium Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Organism="Homo sapiens"
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/lab_host="DH10B"
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US-10-082-502-20 (1-162) x BM832888 (1-591)

Percent Similarity:
Best Local Similarity:
Query Match:

6.28e-103 848.00 100.00% 100.00% 100.00%

Conservative: Mismatches: Indels: Length: Matches:

591 162 0

Gaps:

Alignment Scores:

BASE COUNT ORIGIN

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VERSION KEYWORDS SOURCE

ACCESSION

RESULT 3 BI712899

DEFINITION LOCUS

B1712899 1d98f09.y1 | similar to sequence. BI712899 BI712899.1 EST. human.

HR85 islet Homo sapi TR:Q9Y2B0 Q9Y2B0 TYP

611 bp

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GluLeu

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BQ668530
BQ668530 GI:21778777
EST.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2461 row: c column: 06
High quality sequence start: 208
High quality sequence stop: 350.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institutes of Health, Mammalian Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 673)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT_8211118 NIH_MGC_102
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                              196
                                                                                                         /organism="Homo sapiens"
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/lab_host="DH108 (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:4150512"
/clone_1ib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma"
                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match:
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                              NIH-MGC http://mgc.nci.nih.gov/.
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 719)
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/note="organ: brain: Vector: pCMV-SPORT6; Site_1: Not
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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High quality sequence stop: 710.
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//db_xref="taxon:9606"
//clone=!Ib="NIH_MGC_3843209"
//clone_!Ib="NIH_MGC_21"
//tissue_type="choriocarcinoma"
//lab_host="hH10B (phage=resistant)"
//note="Organ: placents; Vector: pOTB7; Site_1: xhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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JOURNAL COMMENT REFERENCE AUTHORS TITLE

Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC

ACCESSION VERSION KEYWORDS

mRNA sequence. BE733900 BE733900.1 GI:10147892 EST.

SOURCE

ORGANISM

Homo sapiens numan .

527 140 120 407 100

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RESULT 6 BE733900

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Tissue Procurement: ATCC
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Contact: Robert Strausberg,
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National Institutes of Health, Mammalian
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DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
CoorI; cDNA made by oligo-dT priming. Directionally
cloned into EcorI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
a 184 c 233 g 144 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4868100"
/clone_lib="NIH_MGC_15"
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                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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quality sequence stop: 739.
Location/Qualifiers
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/lab_host="DH1OB (phage-resistant)"
/lab_host="DH1OB (phage-resistant)"
/lab_host="Dr3n: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/lab_host="Coran: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/lab_host="Laba" vector: potential of the following 5'
/labaptor: GGCACGAG(G). Size-selected >500bp for average
/labaptor: GGCACGAG(G). Size-selected by Ling Hong in
/labaptor: Library constructed by Ling Hong in
/labap
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/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTP
Tissue Procurement: ATCC/DCTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 930)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
                                                                                      http://image.llnl.gov
Plate: LLAM13509 row: i column:
High quality sequence stop: 515.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         5', mRNA sequence.
BQ437660
BQ437660.1 GI:21176736
                                                                                                                                                                                                                                                                                                                                                    BQ437660 930 AGENCOURT_7897085 NIH_MGC_72 5', mRNA sequence.
                                                                                                                                                                                                                                                                                          Homo sapiens
/clone="IMAGE:615938"
/clone_lib="NIH_WCC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sp(
                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
E 1 (bases 1 to 1117)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectio
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs -r@mail.nih.gov
Tissue Procurement: DCTD/DTp
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (Li
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5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://Image.llnl.gov
Plate: LLCM1968 row: C column: 07
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258 c 320 g 239 t 1 others
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/clone_lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
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                    ArgSerGlnAspLeuH1sCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGlu
  ATTGCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCAGAT
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Endocrine Pancreas Consortium
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Mashington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
Endocrine Pancreas Consortium
Harward University, Howard Hughes Medical Institute
Dept_of_Molecular and Cellular Biology, 7 Divinity Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 59)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (hinoue@im.wustl.edu)
Seg primer: -40UP from Gibco
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 617-495-1812
Fax: 617-495-8557
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Other_ESTs: 1d98f09.yl
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Size-selected on agarose gel. Average insert size -lkb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5085832"
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R., Cole,R., Tsagareishvili,R., Williams,T.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN13303 row: a column: 01
                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, Mammalian
Unpublished (1999)
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AGENCOURT_7801623 NIH_MGC_72
5', mRNA sequence.
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                                                                 238
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/tisue__type="melanotic melanoma"
/lab_host="PH10B (phage-resistant)"
/note="Organ: skin; vector: pcMV-SpORT6; Si
Site_2: Sall; Cloned unidirectionally. pri
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                                          E 1 (bases 1 to 783)

S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MC Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sl
TOShiyuki and Plero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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http://image.llnl.gov
Plate: LLAM11666 row: 1 column:
High quality sequence stop: 730.
Location/Qualifiers
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                   mRNA sequence.
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603192905F1 NIH_MGC_95 Homo
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5', mRNA sequence.
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AGENCOURT_7911956 NIH_MGC_68
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/db_xref="taxon:9606"
/clone="IMAGE:5264328"
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/lab_host="DH108"
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Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13197 row: d column: 14
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 868)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collec
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/tlssue_type="large cell carcinoma"
/tlsb_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pcMV-SPORT6;
Site_2: Sall; Cloned unidirectionally. F
Average insert size 1.8 kb. Library cor
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/db_xref="taxon:9606"
/clone="IMAGE:6009949"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), g
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cm.A. Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://inage.llnl.gov
Plate: LLAM10727 row: a column: 09
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National Institutes of Health, Mammalian
Unpublished (1999)
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/clone_lib="NIH_MGC_95"
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/db_xref="taxon:9606"
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Brownstein (NHGRI), Shiraki
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                                            AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisIleSerHisAsp 160
                                                                      GTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAA 678
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Search completed: March 31, 2003, 04:51:11 Job time: 1041.65 secs

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: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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9 US-10-028-072-173
9 US-10-121-049-173
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APPLICANT: Mannion, Jane
APPLICANT: Benson, Darin R.
APPLICANN: Benson, Darin R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SOUTWARE: CORIXA INVENTION DISCLOSURE DATABASE
SEQ ID NO 309
LENGTH: 814
TYPE: DNA
ORGANISM: Homo sapiens
US-09-864-864-309
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APPLICANT: Mitcham, Jenni
APPLICANT: Mitcham, Jenni
APPLICANT: Dillon, Davin
APPLICANT: Dillon, Davin
APPLICANT: Secrist, Heatt
APPLICANT: Lodes, Michael
APPLICANT: Algate, Paul A
APPLICANT: Fling, Steve
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5. US20020102679A1
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Harlocker, Susan I
Dillon, Davin C.
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FILE REFERENCE:
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CURRENT FILING DATE: 2001-12-19
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Gerritsen, Mary E.
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Desnoyers, Luc
Filvaroff, Ellen
                                                                      Watanabe, Colin K
Wood, William
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Stewart, Timothy A.
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60/081203 60/080165

APPLICATION FILING DATE:

NUMBER:

60/079728 3-27

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APPLICATION NUMBER: 6 FILING DATE: 1998-02-

60/079663

FILING DATE:

APPLICATION NU

NUMBER: 60: 1998-03-2

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R APPLICATION NUMBER: R FILING DATE: 1998-04-R FILING DATE: 1998-04-R APPLICATION NUMBER: R APPLICATION NUMBER: R APPLICATION NUMBER: R

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FILING DATE: APPLICATION NUMBER:

APPLICATION NUMBER: FILING DATE: 1998-05

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1998-05-15 1998-05-13 1998-05-13

NUMBER: 60/0: 1998-05-15

R APPLICATION NUMBER: (
R FILING DATE: 1998-05
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/C
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60/084627

APPLICATION NUMBER:

ломыек: 60/083545 1998-04-29

60/084600 5-07

1998-04-28

60/083322

1998-04-24

60/082999 60/081818

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FILING DATE:

NUMBER: 60/084637 1998-05-07

R FILING DATE: 1998-05-1;
R APPLICATION NUMBER: 60-1;
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R APPLICATION NUMBER: 60-2;
R APPLICATION NUMBER: 60-5-2;
R APPLICATION NUMBER: 60-65-2;
R FILING DATE: 1998-05-2;
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NUMBER: 60/0: 1998-05-22

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APPLICATION

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60/088730 60/088026 60/087106 60/086430 60/086414 60/085704 60/085697 60/085579 60/085339 60/085338 60/085323 60/085149

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; ORGANISM: Homo Sapien
US-10-121-049-173
                                                                                                                                                                                                                                                                                                                                                    US-10-082-502-20 (1-162) x US-10-121-049-173 (1-1210)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT EFLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
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                                                                                                                                                                           GATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCCACCTCACAGAG
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                                                                                                                                                                                                                                   GAAATTGCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCA
                                                         CATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTA
                                                                                                                 CTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGAACAGATTGATCCTTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc Filvaroff, Ellen Gao, Wei-Qiang Geritsen, Mary E. Goddard, Audrey Goddwski, Paul J. Gurney, Austin L. Sherwood, Steven Smith, Victoria Stewart, Tinothy A. Tumas, Daniel Watanabe, Colin K Wood, William
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b. US20030022239A1
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US-10-123-904-173
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APPLICANT: Beresini, Mau
APPLICANT: DeForge, Laur
APPLICANT: Desnoyers, Lu
APPLICANT: Desnoyers, Lu
APPLICANT: Gao, Wei Oian
APPLICANT: Gao, Wei Oian
APPLICANT: Gerritsen, Mad
APPLICANT: Gerritsen, Aud;
APPLICANT: Goddward, Audr
APPLICANT: Goddward, Aud;
APPLICANT: Goddward, Ste
APPLICANT: Sherwood, Ste
APPLICANT: Smith, Victor
APPLICANT: Smith, Victor
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-04-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wood, W. APPLICANT: Zhang,
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo
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                                                                       AspGlySerGlnSerValValGluValProTyrAlaArgSerGluAlaHisLeuThrGlu
                                                                                                                             GluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
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CTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGGAACAGATTGATCCTTCCACC
                                                        GATGGCAGCCAGTCAGTGGGAGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAG
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Wood,William
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o. US20030022328A1
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Matches:
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Pred. No.:
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US-10-140-470-173
; Sequence 173, Application US/10140470
                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: HOMO
US-10-140-470-173
                                                                                           US-10-082-502-20 (1-162) x US-10-140-470-173 (1-1210)
                                                                                                                                          Percent Similarity:
Best Local Similarity:
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APPLICANT: Beresti
APPLICANT: DeForg
APPLICANT: Desnoy,
APPLICANT: Filvar,
APPLICANT: Gao, We
APPLICANT: Gao, We
APPLICANT: Goddar
APPLICANT: Goddar
APPLICANT: Godows
APPLICANT: Gurney
APPLICANT: Sterwo
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APPLICANT: Stewar
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CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or F1
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
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                                                                                                                                Match:
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ArgArgSerGlnAspLeuH1sCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
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                                              CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGG
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Tinothy A.
Tumas, Daniel
Watanabe, Colin K
Wood, William
Whood, William
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Filvaroff, Ellen
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Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
ORGANISM: Homo Sapien
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US-10-082-502-20 (1-162) x US-10-175-746-173 (1-1210)
                                           Query Match:
                                                       Percent Similarity:
Best Local Similarity:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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Wood, William
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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Alignment Scores: Pred. No.:
                                    ; ORGANISM: Homo US-10-176-918-173
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                                                                     Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 173, Publication No
                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                      CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
                                               TYPE: DNA ORGANISM:
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A
Tumas, Daniel
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Gerritsen, Mary E.
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Filvaroff, Ellen
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                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACLDS ENCODING THE SAME FILE REFERENCE: P9330R1C288

CURRENT APPLICATION NUMBER: US/10/176,921

CURRENT FILING DATE: 2002-06-20
                                                                                                        APPLICANT:
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APPLICANT: Beresini, Ma
APPLICANT: DeForge, Lau
APPLICANT: Desnoyers, I
Prior Application removed NUMBER OF SEQ ID NOS: 550
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                                                                                               Stewart, Timothy
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Filvaroff, Ellen
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US-10-137-865-173

Sequence 173, Application US/10137865

Publication No. US20030032155A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Desnoyers Luc

APPLICANT: Desnoyers Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Genvieren, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddowski, Paul J.

APPLICANT: Godnowski, Paul J.

APPLICANT: Sherwood, Steven
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; ORGANISM: Homo
US-10-176-921-173
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Pred. No.:
                               APPLICANT:
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; PILOT APPLICATION removed - See Palm or File Wrap
; NUMBER OF SEQ ID NOS: 550
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 173
; LENGTH: 1210
; TYPE: DNA
COCANTEN: Homo Sanien
Sequence 173, Application US
Publication No. US2003003215
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Tivaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
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Desnoyers, Luc
Filvaroff, Ellen
                                                       Beresini, Maureen
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Gao, Wei-Qiang Gerritsen, Mary

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RESULT 11
US-10-142-431-173
; Sequence 173, Application US/10142431
; Publication No. US20030036179A1
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LENGTH: 1210
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
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ORGANISM: Homo Sapien
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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CURRENT FILING DATE: 2002-05-10
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                                                        ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
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Gerritsen, Mary I
Goddard, Audrey
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Gurney, Austin L.
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CURRENT APPLICATION NUMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
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APPLICANT: Beresini, Mauro
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Gurney, Austin L.
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NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C59
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
TYPE: DNA
ORGANISM: Homo Sapien
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Best Local Similarity:
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C244
CURRENT APPLICATION NUMBER: US/10/142,419
CURRENT FILING DATE: 2002-05-10
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Gerritsen, Mary E.
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; SEQ ID NO 173
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-262-173
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                                          Query Match:
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary
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CURRENT FILING DATE: 2002-04-15
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-DB-ISSUED_PATENTS_NA -OFMT-fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZES-00 -MINLEN=0 -MAXLEN=200000000
-USER-US10082502_eGGN_1_131_erunat_24032003_135100_6616 -NCPU=6 -ICPU=3
-MO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/6B_COMB.seq:*
/cgn2_6/ptodata/1/lna/6B_COMB.seq:*
/cgn2_6/ptodata/1/lna/backfiles1.seq:*
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US-09-163-285-1

US-09-724-864-14

US-08-257-073-10

US-08-961-083-159

US-08-971-152A-1

US-09-071-035-3

US-09-071-035-1

US-08-961-527-208

US-08-961-527-208

US-08-961-527-103
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Sequence 3, Appli
Sequence 1, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 159, Appl
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 208, App
Sequence 208, Appli
Sequence 21, Appli
Sequence 24, Appli
Sequence 103, App
                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-163-285-3
; Sequence 3, Application US/09163285
; Patent No. 6204013
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Khodadoust
TITLE OF INVENTION: N
TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                     SOFTWARE:
              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                             02109
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              (617)742-4214
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			Sequence 38, App Sequence 38, App Sequence 38, App Sequence 38, App Sequence 38, App Sequence 38, App	Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Patent NO. 535245 Sequence 2, Appl Sequence 1, Appl Sequence 3, Appl Sequence 3, Appl	
	71 8.4 2160 2 US-08-840-236-2 Sequence 71 8.4 2160 2 US-08-9505-248A-2 Sequence 71 8.4 2160 2 US-08-505-448A-5 Sequence 71 8.4 2160 2 US-08-505-448A-5 Sequence	71.5 8.4 676 4 US-08-676-444-41 Sequence 71.5 8.4 676 4 US-08-998-416-1130 Sequence 71.5 8.4 676 4 US-08-998-416-1130 Sequence 71.5 8.4 1708 4 US-08-998-416-238 Sequence 71.5 8.4 2160 2 US-08-840-236-2 Sequence 71 8.4 2160 2 US-08-840-236-5 Sequence 71 8.4 2160 2 US-08-840-236-5 Sequence 71 8.4 2160 2 US-08-840-236-5 Sequence 71 8.4 2160 2 US-08-505-448A-5 Sequence 71 8.4 2160 2 US-08-505-448A-5 Sequence	73 8.6 4131 3 US-09-139-491-38 Sequence 73 8.6 4131 5 PCT-US92-0322-38 Sequence 72.5 8.5 4371 1 US-08-803-973-1 Sequence 72.5 8.5 4371 1 US-08-803-972-1 Sequence 72.5 8.5 1640 4 US-08-803-972-1 Sequence 71.5 8.4 676 4 US-08-998-416-1130 Sequence 71.5 8.4 41708 4 US-09-998-416-1130 Sequence 71.5 8.4 2160 2 US-09-470-512A-3 Sequence 71 8.4 2160 2 US-08-840-236-5 Sequence 71 8.4 2160 2 US-08-505-448A-5 Sequence	73 8.6 4131 1 US-07-972-644-38 Sequence 73 8.6 4131 1 US-08-297-949-38 Sequence 73 8.6 4131 1 US-08-297-510-38 Sequence 73 8.6 4131 1 US-08-479-532-38 Sequence 73 8.6 4131 1 US-08-455-526-38 Sequence 73 8.6 4131 1 US-08-455-526-38 Sequence 73 8.6 4131 1 US-08-455-525-38 Sequence 73 8.6 4131 3 US-09-139-491-38 Sequence 73 8.6 4131 5 PCT-US92-03222-38 Sequence 72.5 8.5 4371 1 US-08-803-972-1 Sequence 72.5 8.5 4371 1 US-08-803-972-1 Sequence 72.5 8.5 1640 4 US-08-998-416-1130 Sequence 73. 8.4 4774 4 US-08-998-416-928 Sequence 74. 8.4 41708 4 US-08-998-416-928 Sequence 75. 8.4 47708 4 US-09-998-416-928 Sequence 76. 8.4 2160 2 US-08-840-236-5 Sequence 77. 8.4 2160 2 US-08-840-236-5 Sequence 78. 8.4 2160 2 US-08-840-236-5 Sequence 79. 8.4 2160 2 US-08-8505-448A-5 Sequence	3372 3 US-09-344-521-1 5 8.8 3372 4 US-09-280-598-1 5 8.8 5177 6 5352450-1 74 8.7 5661 4 US-08-938-105-2 8.7 1776 1 US-08-938-105-2 8.7 1776 1 US-08-938-105-2 8.7 1776 1 US-08-92-2298-1 5 8.7 1776 1 US-08-22-2298-1 5 8.6 2012 2 US-09-102-433-1 8.6 4131 1 US-09-124-33-1 8.6 4131 1 US-08-297-494-38 8.6 4131 1 US-08-297-494-38 8.6 4131 1 US-08-297-510-38 8.6 4131 1 US-08-479-532-38 8.6 4131 1 US-08-479-532-38 8.6 4131 1 US-08-479-532-38 8.6 4131 1 US-08-455-525-38 8.6 4131 1 US-08-455-525-38 8.6 4131 1 US-08-455-525-38 8.6 4131 1 US-08-03-973-1 8.6 4131 3 US-08-03-973-1 8.6 4131 3 US-08-03-973-1 8.7 431 1 US-08-03-973-1 8.8 4131 1 US-08-03-973-1 8.9 4131 1 US-08-03-144-41 8 5 90-03-144-41 8 6 90-04-146-1130 8 6 90-04-03-128-3 8 8 90-06-02 8 90-08-03-94-16-1130 8 90-08-03-94-16-2101 8 90-08-03-94-16-2101 90-08-

ALIGNMENTS

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APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
CCOUNTRY: USA
ZIP: 02109
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/163,285
CURRENT APPLICATION NUMBER: US/09/163,285
FILING DATE: June 24, 1998
APPLICATION NUMBER: 60/090,398
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: MNI-049
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)42-4214
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                         Sequence 1, Application US/09163285
Patent No. 6204013
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                          ZIP: 02109
                                                                                                                                                       STREET:
                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaGlnValAsp---
                                                                                                                                                                                                                                                                                                                                                                                                  GTGGGAGACTGGTACTTCCACCATCAGGAGCAGCCCCTACAAAATTTTCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGAGGTCACATACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATT 498
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                                                                                                                 Massachusetts
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Matches:
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RESULT 3
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; LOCATION:
US-09-163-285-1
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APPLICATION UMBER: 60/090,39
FILING DATE: JUNE 24, 1998
ATTORNEY/AGENT INFORMATION:
NAME: MANDICAGOUTAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPAN: (617)227-7400
TELEPAN: (617)42-4214
INFORMATION FOR SEQ ID NO: 1:
Sequence 14, Application US/09724864 Patent No. 6380362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDN FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/163,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                  128 LeuIleGlu---PhePheSerArgGluAlaAspAsnValLysAspLysLeuCys 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 ProLysLysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSerVal 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                               GTGGAGGTCACATACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspArgMetLysGluTyrGlyGluGlnIleAspProSerThrHis-----ArgLysAsn 84
                                                                                                                                                                                                                                                                                               AspLeuGlnGlyIleArgIleAspSerAspIleSer-----
                                                                                                                                                                                                                                                                                                                                                                               TyrValArgValValGlyArgAsnGlyGluSerSerGlu-----Leu 98
                                                                                                                                                                                                                                                                                                                                                                                                                    GAGCGGATCCTGGACTAT------AGTGTTCACGCTGAGCGCAAGGGC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAGAGAATTTATGT 406
                                                                                                   GTGGGAGACTGGTACTTCCACCATCAGGAGCAGCCCCCTACAAAATTTTCTCTGT
                                                                                                                                                                                                                    -----GlyThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGlu 127
                                                                                                                                                                                                                                                           GTGCAGAAGGGGGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGC
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Indels:
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APPLICANT: Watson, James G.

APPLICANT: Murison, James G.

TITLE OF INVENTION: Polynucleotides, polypeptides expressed

TITLE OF INVENTION: Polynucleotides and methods for their use.

FILE REFERENCE: 11000.1050U1

CURRENT FALLING DATE: 1200-11-28

PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0
  Sequence 10, Application U
Patent No. 5766597
GENERAL INFORMATION:
APPLICANT: De Taisne,
APPLICANT: Tine, John
TITLE OF INVENTION: MA
                                                                                                                                      RESULT 4
US-08-257-073-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-082-502-20 (1-162) x US-09-724-864-14 (1-915)
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 TyrValArgValValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArg 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 CysAspArg---MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsn 84
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                                                                                                                                                                                                                                HisAspGluLeu 162
                                                                                                                                                                                                                                                                                                ValLysAspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisIleSer 158
                                                                                                                                                                                                                                                                                                                                                                        IleValGluGluTyr---GluAspGluLeuIleGluPhePheSerArgGluAlaAspAsn 138
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                                    Paoletti, Enzo
de Taisne, Cha
                        John A.
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Matches:
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US-10-082-502-20 (1-162) x US-08-257-073-10 (1-5181)
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TELEFAX: (212) 840-0712
TELEY: 42506 CURTMS
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
                                    1432 GATAATAAGGAAAGAAAATATTCATTAATAACATTAAAAAAACAAATTGATTTAGAAGAA 1491
                                                                                                               1372 TCATATGGTGATTTAATGAATCCTGATACTAAAGAAAAATTAATGAAAAAATTATTACA 1431
                                                                                                                                                                                                                                                                                                                                             1192 GATCCACTTGAATTAGAATATTATTTAAGAGAAAAAAATAAAAAAGTTGATGTAACACCT 1251
                                                                                                                                                                                                                                                                    1252 AAATCACAAGATCCTACGAAATCTGTTCAAATACCAAAAGTTCCTTATCCAAATGGTATT 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
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CORRESPONDENCE ADDRESS:
103 IleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIleValGlu 122
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                                                                                                                                                    71 GluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgValValGly 90
                                                                                                                                                                                                                             56 AlaHis-----LeuThrGluLeuLeuGluGluIleCys-----AspArgMetLys 70
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TOPOLOGY: 11r
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 5181 base pairs
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STREET: 5
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                                                                                                                                                                                         GTATATCCTTTACCACTCACTGATATTCATAATTCATTAGCTGCAGATAATGATAAAAAT 137;
                                                                                                                                                                                                                                                                                                                                                                                  AspGluLeuGluTrpGluTleAlaGlnValAspProLysLysThrIleGlnMetGlySer
                                                                                   ArgAsnGlyGlu-----
                                                                                                                                                                                                                                                                                                      PheArgIleAsnProAspGlySerGlnSerValValGluValProTyrAlaArgSerGlu 55
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530 Fifth Avenue,
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SYSTEM: PC-DOS/MS-DOS
PATCHIN Release #1.0, Version
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09-JUN-1994
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25th Floor
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                                                                         -----SerSerGluLeuAspLeuGlnGly 102
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Matches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BIOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1492 AAAAAAATTAATCAC------ACAAAAGAACAAAATAAAAAATTACTTGAA 1536
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                          575 ATTTCTACTTTGGAACAAGAAGTTGCTACTGCTCAACATCAAGTAGATAATTTGAAAAAA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 AlaAspAsn-----------ValLysAspLysLeuCysSerLysArg 147
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51 TyralaArgSerGluAlaHisLeuThrGluLeuLeuGluGluIleCysAspArgMetLys 70 ::: ||||||
                                                                                     31 IleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSerValValGluValPro 50
                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                     CTTCTTGCTGGTGCG-----GATCCTGATGATGGCACAGAAGTTATAGAAGCTAAA 685
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GATTATGAAAAGTCAAAAAAGGATTATGAAGAATTACTTGAAAAATTTTATGAAATGAAA 1596
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9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1924 base pairs
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RESULT 6
US-08-750-152A-1
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APPLICANT: ASAKUR
APPLICANT: KIMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 1:
                                   FEATURE:
                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOUTWARE: PastEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4394 base pair
                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     956 ACTAAAAAAGCTGAATTG 973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GlyThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeuIleGlu 130
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TELEPH
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                                                                  STRAIN: ATCC13869
                                                                                                             ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 22152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 GluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgValValGly 90
NAME/KEY:
                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACTTGAAAAACTTCTTGACAGCCTTGATCCTGAAGGTAAGACTCAGGATGAATTAGAT 805
                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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Sdo
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                                                                                                         Brevibacterium lactofermetum
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LOCATION: FEATURE:

; FEATURE: ; NAME/KEY: ; LOCATION: US-08-750-152A-1

FEATURE: NAME/KEY:

LOCATION: NAME/KEY:

LOCATION:

FEATURE:

NAME/KEY:

Alignment Scores:

No.:

Query Match:

Best Local Similarity: Percent Similarity:

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US-10-082-502-20 (1-162) x US-08-750-152A-1 (1-4394)
                                                                                                                                                              Sequence 3, Application US/09071035
Patent NO. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus
NUMBER OF SEQUENCES: 496
                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                         3008 GGCATCACCGGCTCCCAGAAGCTTCCACACGGCCTTGAGACCAACATCTCCCCGTGAAGAG
                                                                                                                                               CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleGluPhePheSerArgGluAlaAspAsnValLysAspLysLeuCysSerLysArgThr 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCTCCAACGAA-----GATGCAGAAGCAGTCGTCCGCGACTTCCACGACCAGATG
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                                                                                                             E: Human Genome Sciences, Inc.
9410 Key West Avenue
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4243..4281
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281..287
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Matches:
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RESULT 8
US-09-071-035-1
Sequence 1, Application US/09071035;
Patent No. 6448043
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                     707 GATAAA 712
                                                                                                                                                    139 ValLys 140
                                                                                                                                                                                            647
                                                                                                                                                                                                                             119
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                                                                                                                                                                                                                                                                                                                          530 AACAAAGAAGTCGTTGGTGCTGGTTTTGACTCGTTAAATAACTATTACGCAATTGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                          473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422
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                                                                                                                                                                                                                                                                                                                                                              85 TyrValArgValValGlyArgAsnGlyGluSerSerGlu-----Leu
                                                                                                                                                                                                                                                                                                                                                                                                                               76 IleAspProSerThr------HisArgLysAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                  GAAGTCGTGGACTATTACCGTGATGGTATCGAAGCAGGTTACTTCCGCACAGCTGGTTCA
                                                                                                                                                                                                                                                       AAAAACAAAGGCGTTGATTTTAATAAAGACTTAGATTTAACAAGCAAAGATTCA---CAA
                                                                                                                                                                                                                                                                                                                                                                                               GTA---CCGAAAACATTAGAGGAATTAAAAGAAGCTTCTAAAACAATTTACGAAAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerIleValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsn 138
                                                                                                                                                                                                                                                                                     AspLeuGlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLyspheAlaCysGlu 118
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CITY: Rockville STATE: Maryland

COUNTRY:

20850 Maryland Y: USA STREET:

ADDRESSEE:

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Best Local Similarity:
Query Match:
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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SerIleValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsn 138
                                           AAAAACAAAGGCGTTGATTTAATAAAGACTTAGATTTAACAAGCAAAGATTCA---CAA
                                                                                                                             TyrValArgValValGlyArgAsnGlyGluSerSerGlu---
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                                                                       AspLeuGlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGlu 118
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APPLICANT: Charle
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
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ATTORNEY/AGENT INFORMATION:
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CITY: Rockville
STATE: Maryland
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                              GluTyrGlyGluGlnIleAspProSerThrH1sArgLysAsnTyrValArgValValGly 90
                                                               TyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluIleCysAspArgMetLys 70
                                                                                                                                   CTTCTTGCTGGTGCG-----GATCCTGATGATGGCACAGAAGTTATAGAAGCTAAA 811
GAACTTGAAAAACTTCTTGACAGCCTTGATCCTGAAGGTAAGACTCAGGATGAATTAGAT 931
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97 GluLeuAspLeuGlnGlyIleArgTleAspSerAspIleSerGlyThrLeuLysphe 115	42 GlySerGlnSerValValGluValProTyrAlaArgSerGluAlaH15LeuThrGluLeu 61 1324 TCCAAATACCAACAGATCAAGTTGTCAAAGAAGATAAT 1362 62 LeuGluGluIleCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThH18 81 :::! ::::	10-082- 22 1276	Alignment Scores: Pred. No.: 77.50 Percent Similarity: 1.298 Best Local Similarity: 20.658 Ouery Match: 9.148 DB: Length: 2508 Antches: 32 Conservative: 32 Conservative: 35 Indels: 35 Gaps: 8	US-08-850-993-1 US-08-850-993-1 Sequence 1, Application US/08850993 Patent NO. 5955277 GENERAL INFORMATION: APPLICANT: Hansen, Torben APPLICANT: Hansen, Torben APPLICANT: Pedersen, Oluf B. TITLE OF INVENTION: Mutant cDNA Encoding The p85alpha TITLE OF INVENTION: Subunit Of Phosphatidylinositol 3-Kinase FILE REFERENCE: 4802-200-US CURRENT APPLICATION NUMBER: US/08/850,993 CURRENT FILING DATE: 1997-05-05 EARLIER APPLICATION NUMBER: 0539/96 EARLIER FILING DATE: 1996-05-06 NUMBER OF SEO ID NOS: 25 SOSTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 2508 TYPE: DNA ORGANISM: human	145 SerLysArgThrAspLeu 150 . ::: ::: ::: 1082 GCTAAAAAAAGCTGAGTTA 1099	91 ArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAspIleSer 110 ::: :::
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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FELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 4865 base pairs
TYPE: nucleic acid
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TOPOLOGY: line
MOLECULE TYPE: G
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APPLICANT: Kelly, Charles
TITLE OF INVENTION: POLYPEPTIDE FRAGMENTS CAPABLE
TITLE OF INVENTION: OF COMPETITION WITH STREPTOCOCCUS MUTANS ANTIGEN I/II
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
ADDRESSEE: MORRISON & FOERSTER
COMPETER: 2000 December 1970 Avenue, NW. suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
320 CTGAACAAAGTCAAACCAAGCTGGAGAGACAAATGGTTCATACCATTGAAGTACCTAAAA 379
                                                                 1579 CGTGAAGGCAATGAGAAAGAAATACAAAGGATTATGCATAATTATGATAAGTTGAAGTCT 1638
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                       146 LysArgThrAspLeuCysAspHisAlaLeuHisIleSerHisAsp 160
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CITY: Washington
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                                                                                                   US-10-082-502-20 (1-162) x US-08-961-527-103 (1-5558)
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US-08-961-527-103
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 103, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     550 CAATATAAATCGGATGTAGCTGCTCATGAGGCAGAAGTTGCT 591
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                                                      14 LeuValAspGluLeu-------GluTrpGluIleAlaGlnValAspProLys 28
                                                                                                                                                                                                                                                                                                               LENGTH: 5558 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 ValValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIle-----
29 LysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSerValValGlu 48
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	MOLECULE TYPE: DNA (genomic) FEATURE:	MOLE FEAT	٠. ٠.
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	TELEPHONE: 301-309-8504	TE	٠
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	REGISTRATION NUMBER: 36,373	RH	•• ••
	Y/AGENT INFORM	ATTC	
	FILING DATE: 11-APR-1996	F	٠
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	CLASSIFICATION: 435	ជ:	
	APPLICATION NUMBER: US/08/837,029	F AF	
	APPLICATION DATA:	CURRENT	
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	MEDIUM TYPE: Floopy disk	ME COME	
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	COUNTRY: US	25	
	CITY: KOCKVILLE	3 5	
	410 Key West Avenue	ខ្ម	٠.
	n Genom	AL	
	NUMBER OF SEQUENCES: 8	CORE	
	 #	TITLE	
	APPLICANT: Wei et al.	GENER	
	o. 5945303	Patent N	
	029-	US-08-837	
		RESULT 13	т.
		Db 2514	-
	5 LysArgThrAspLeuCysAspHisAlaLeuHisIleSerHisAspGluLeu 162	Qy 146	_
2513	TTCAGCCATTTTCATATAGAGGTCATTGATACGAGCTTCAGCTTTGAAAAG	Db 2454	н
145	lAspLysLeuCysSer	Qy 141	_
2453	3CATGAGAGCATCAACATCCGCGCCGTC	Db 2418	-
4	0+4+]+0+4110p0+4104+400+		
5		Ov 133	,
2417		Db 2379	_
122	IleArgIleAs	Оу 103	_
2378	CATGCCAAAGTCCATAACACCAAGAGCACGCGCTACTTCGT	Db 2319	п
102	ValGlyArgAsnGlyGluSerSerGluLeuAspLeuGlnGly	Qу 89	_
2318		Db 2268	_
88	<pre>MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgVal</pre>	Ωу 69	
2267	GTTGGTCGGCTCGTCCAACAGCAAGATATCAGGCTTTTCAAGGAGAAGTTTTGC	Db 2214	н.
83	ValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGl	Оу 49	_
2213	GGCATTCTCATAGTTTTGGAGATAGCGCTTGAGCCAATCAAT	Db 2154	

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RESULT 14
US-07-906-349A-1
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Query Match:
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                                                 Sequence 1, Application US/07906349A

Patent No. 5434064

GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: TARGET PROTEINS
TITLE OF INVENTION: TARGET PROTEINS
TITLE OF INVENTION: TARGET PROTEINS
CORRESSEE: BETWAY AND NESSEE:
ADDRESSEE: ADDRESSE: 419 Seventh Street, N.W.
STREET: 419 Seventh Street, N.W.
STREET: Mashington
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FEATURE:
NAME/KEY:
LOCATION:
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Matches:
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RESULT 15
US-08-167-035-1
; Sequence 1, Application US/08167035
; Patent No. 5618691
· GENERAL INFORMATION:
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US-10-082-502-20 (1-162) x US-07-906-349A-1 (1-3372)
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Best Local Similarity:
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TELEPACE 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3372 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1279 CTAGCTCAGTATAATCCCAAATTGGATGTGAAATTA------CTTTATCCAGTA 1326
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                  146 LysArgThrAspLeuCysAspHisAlaLeuHisIleSerHisAsp 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 07/643,237
FILING DATE: 18-JAN-1991
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LeuGluGluIleCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThrH1s 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 IleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnProAsp ::::|||||| :::: |||
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CGAATCAGTGAAATTATTGACAGTAGAAGAAGATTGGAAGAAGAC 1686
                                                                                                                 CGTGAAGGCAATGAGAAAGAAATACAAAGGATTATGCATAATTATGATAAGTTGAAGTCT
                                                                                                                                                            GAAGAACAGTGCCAGACC---CAAGAGCGGTACAGCAAAGAATACATAGAAAAGTTTAAA
                                                                                                                                                                                                -----AlaCysGluSerIleValGluGluTyrGluAspGluLeuIleGluPhePheSer 133
                                                                                                                                                                                                                                         GluLeuAspLeuGlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPhe---
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Best Local Similarity:
Query Match:
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FILING DATE: 16-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-062
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                       1366 ATTGAAGCTGTAGGGAAAAAATTACATGAATATAACACTCAGTTTCAAGAAAAAAGTCGA 1425
                                                                                                                                                                                                          1327 TCCAAA-----TACCAACAGGATCAAGTTGTCAAAGAAGATAAT 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3372 base pairs
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                                                                    1426 GAATATGATAGATTATATGAAGAATATACCCGCACA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                   TELEFAX: (212) 869-9
                                                                                                                                                                                                                                             42 GlySerGlnSerValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeu 61
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TOPOLOGY: unl
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Skolnick, Edward Y.
Margolis, Benjamin L.
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Search completed: March 31, 2003, 04:26:11 Job time : 42.3198 secs

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-DB=N_Geneseq_101002 -QFMT-fastap -SUFFIX=rng -MINMARCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -STRATF-1 -END--1 -MATRIX-biosum62 -TRANS-buman40.cd1
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTENT-pto -NORM-ext -HEARSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US10082502_GCGN_1_1_741_Grunat_24032003_135058_6538 -NCPU-6 -ICPU-3
-NO_MINLENY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -NAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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RESULT 1 AAZ38326 AAZ38326 standard; cDNA; 546 BP. XX AC AAZ38326; XX DT O9-FEB-2000 (first entry) XX KW HUMAN transmembrane protein cDNA clone HP10390 coding sequence. XX KW HP10390; transmembrane domain; stomach cancer cell; antibody; KW assay reagent; diagnostic marker; primer; probe; antisense; gene therapy; XX XX XX SS Homo sapiens. XX FH Key Location/Qualifiers 1.540

ALIGNMENTS

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                     HP10390 which encodes a 20 kD protein with one putative transmembrane domain in the N-terminus. The cDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically.
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(PROT-)
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                  GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle
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/product= "Human transmembrane protein HP10390"
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03-JUL-1997;
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03-JUL-1997;
19-MAY-1998;
19-MAY-1998;
17-JUN-1998;
This cDNA clone encodes human secretory peptide-9, or Zsig9, variant (see AAW88474). Zsig9 (see also AAW88469) is overexpressed human brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors. Thus, Zsig can be used as an indicator for cancer. Zsig9 cDNA was discovered in a placenta clone from a full-term pregnancy cDNA library which contained an expressed sequence tag (see AAX06971). The invention provides polynucleotides (see AAX06968-70) encoding Zsig9 polypeptides (see AAX06977) including manture polypeptides, other processed forms, variants and mouse orthologues. The Zsig9 gene, or probes derived from it, can be used to determine if Zsig9 is present on chromosome
                                                                                                                                        Claim
                                                                                                                                                                      New mammalian secretory peptide-9 (Zsig9) - enhancer for placenta, liver and heart, and
                                                                                                                                                                                                       WPI; 1999-106055/09
P-PSDB; AAW88474.
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                                                                                                                                      2; Page 73-74; 85pp; English
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        Secretory protein-9; Human zsig9; chromosome 12q15 region; variant; overexpression; antagonist; antibody; antisense nucleotide; tumour; treatment; receptor; radio-label; fusion; polypeptide toxin; technique; down-regulation; probe; diagnostic; therapeutic; cancer; brain; liver; detection; stomach; lymphoma; alternative splicing; allelic variation;
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                                                                                                                        The present DNA sequence is a gene encoding the variant of the secretory protein-9, Zsig9 that arises due to alternative splicing, allelic variation or silent mutations that result in amino acid changes. This sequence is mapped to the human chromosome 12q15 region. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to Zsig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to Zsig9 and it may be radiolabelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of Zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding Zsig9. The Zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma,
                                                                                                                                                                                                                                                                                                                                               WPI;
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This sequence represents the human cDNA clone HP10390 which encodes a 20 kD protein with one putative transmembrane domain in the N-terminus. The CDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, assay reagents, as diagnostic tissue markers, for the isolation of
                                                                                                                                                                                                                             Human proteins with transmembrane domains, proliferation and differentiation, useful finflammation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically.
                                                             cytotoxic
                                                                                                                        ABK52765;
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                                                                                                                                        standard; cDNA;
                                                   sequence tag; EST; human; c:
T lymphocyte; chemotherapy;
rane protein 4; gene; ss.
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y; cytostatic; chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to modulators of a cancer-related genes. Also CC described are: (1) processes for identifying an anti-neoplastic agents CC comprising contacting a cell exhibiting neoplastic activity with a CC compound first identified as a cancer related gene modulator, and CC compound first identified as a cancer related gene modulator, and CC detecting a decrease in the neoplastic activity. (2) a process for CC determining the cancerous state of a cell by determining an increase in CC the level of expression of at least one gene, where an elevated CC expression relative to a known non-cancerous cell indicates a cancerous CC state or potentially cancerous state. The anti-neoplastic agent is CC useful for treating cancer or for protecting an animal against cancer. CC The immunogenic composition is also useful for treating cancer in an CC animal, where the composition elicits the production of cytotoxic TC complosition should be a human. The cancer-linked genes and polypeptides are also CC useful as targets for cancer therapy or chemotherapy. The present CC sequence represents a cancer-linked genes and polypeptides are also cancer transmembrane acceptance in a cancer of the context 
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12-OCT-2000;
12-OCT-2000;
16-OCT-2000;
19-OCT-2000;
19-OCT-2000;
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2000US-244932P.
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Antibody preparation by inoculation of an animal with a vector expressing a fusion protein of an antigen on the C-terminal side transmembrane domain for use as drugs, diagnostic reagents and
                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence
                                                                                                                                                                Kato
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24-AUG-2000; 2000JP-0254407
                                                                                                                                                                                                                                                                            WO200208416-A1.
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                                                            Example;
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                                                                                laboratory reagents
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)B; ABB09717.
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                                                                                                                                                              Nagata N,
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The specification describes a method of antibody preparation. The method comprises inoculating an animal with a vector expressing a fusion protein having an antigen protein fused to the C-terminal side (extracellular) of a transmembrane domain protein (the

intracellular),

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 purifying the antibody from the animal. The antibodies can be used
as drugs, vaccines, diagnostic reagents and laboratory reagents. The
present sequence encodes a polypeptide, designated HP10390, which was
used in the course of the invention.
 23-MAY-2001;
             29-NOV-2001.
                           WO200190154-A2
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Pred. No.:
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13-JUN-2000; 2000US-213673P.
21-JUN-2000; 2000US-213673P.
03-AUG-2000; 2000US-223288P.
01-MAR-2001; 2001US-272790P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide encoding polypeptide comprising ovarian tumour protein, useful for detection, diagnosis and human ovarian cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 253-254; 285pp; English
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The invention relates to nucleic acid sequences (AAX22111 to AAX22134) CC encoding human secreted proteins (AAV01135 to AAX01135). The secreted protein gene sequences are deposited with the ATCC under deposit number ATCC 209118. Host cells comprising recombinant vectors containing the cc nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a cc sample or by determining the amount of the new polypeptides in a cc polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developmental abnormalities and foetal deficiencies, autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders, autoimmune diseases, immune deficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-1997;
01-JUL-1997;
01-JUL-1997;
12-SEP-1997;
                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, immune deficiency diseases or blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; gene therapy; protein therapy; tissue; cance; tumour; neurodegenerative disorder; leukaemia; autoimmune disease; Alli developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; schizophrenia; immunological disorder; mood disorder; memune deficiency disease; respiratory disorder; arthritis; skeletal; haematopoitetic disorder; neural, osteoporosis; metabolic disorder; cardiovascular; endocrine; gastrointestinal; asthma; diagnosis; ds.
                                                                                                                                                                                                                                                                   Claim 4; Page
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97US-0051381.
97US-0051480.
97US-0058598.
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Homo

breast; prostate; cervical; tumour necro cartilage; ear; proliferation; glucose; adipocyte; A-peptide; factor VIIA; gene

nd transmembrane; PRO; mammalian; cancer; lung; cervical; tumour necrosis factor-alpha; TNF-alpha; roliferation; glucose; free fatty acid; skeletal muide; factor VIIA; gene therapy; ss.

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for PRO4426

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24-OCT-2001 AAS21330;

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01-DEC-2000;

2000WO-US32678

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CC AAS21244-AAS21518 encode for novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CPRO polypeptides, to link bloactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, recttal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the cartilage, the proliferation of chondrocytes, the proliferation or coartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide complexities can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, can be completed in an analysis of the properties can be used in gene therapy.
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P-PSDB; AAU12258.
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2000WO-US00376

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2000WO-US04342

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2000WO-US04914

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A, Godowski PJ, Gurney AL, Sherwood :
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04-SEP-1998;
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17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
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97US-0069957.
98US-0074121.
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98US-0096116.
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                                         RESULT 11
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                   AAX06970 standard; cDNA; 1069
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                                                                                                                                                    H18ArgLysAsnTyrValArgValValGlyArgAsnGlyGluSerSerGluLeuAspLeu
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This cDNA clone encodes novel mouse secretory peptide-9, or 2sig9 (see AAW88476), an orthologue of novel human Zsig9 (see AAW88469). Chuman Zsig9 is overexpressed in a number of tumours including brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors, and thus can be used as an indicator for cancer. The invention provides polynucleotides (see AAW86469-70) encoding Zsig9 polypeptides (see AAW86469-77) including mature polypeptides, other processed forms, variants and the mouse orthologues. The Zsig9 gene, or probes derived from it, can be contained and colored as diagnostic agents to determine the presence of zsig9 and thus the presence of cancer. They can also be labelled with tradicisotopes or fused with toxins and used to treat tumours which overexpress Zsig9. Antisense nucleotides derived from Zsig9 colored colored can be used to inhibit the growth of tumour cells. Zsig9 colored can be used to enhance the growth or development of the
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19-MAY-1998;
19-MAY-1998;
17-JUN-1998;
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P-PSDB; AAW88476.
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                                                                                          Sequence 1069
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98US-0085983.
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358..417
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an indicator
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Conservative: Mismatches: Indels:

US-10-082-502-20 (1-162) x AAX06970 (1-1069)

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RESULT 12
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                                                                                                                                                                       Secretory protein-9; mouse Zsig9; ortholog; overexpression; antibody; antisense nucleotide; tumour; treatment; receptor; radio-label; polypeptide toxin; down-regulation; diagnostic; therapeutic; probe; cancer; brain; liver; detection; stomach
                                                                       mat_peptide
                                                                                                                                                                                                                                   07-FEB-2000
       19-MAY-1999;
                        25-NOV-1999.
                                        WO9960405-A1
                                                                                       sig_peptide
                                                                                                                                                  Mus musculus
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       99WO-US11107
                                                               /*tag= 1
418.903
/*tag= 0
                                                                                       "tag" a
/*tag" a
/product= "Mouse Zsig9 secretory protein"
/note= "Overexpressed in tumours"
358..417
                                                                                                                        Location/Qualifiers
358..906
                                                        /label=
                                                                                                                                                                                                                                                                   DNA; 1069
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                                                       Mature_Zsig9_protein_variant-4
                                                                                                                                                                                                                 Zsig9 secretory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present DNA sequence is an ortholog encoding the secretory protein-9, zsig9 derived from mouse. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to Zsig9 are unseful for detecting and treating tumours. The antagonist may be an antibody or receptor to zsig9 and it may be radio-labelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of Zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding Zsig9. The Zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma etc., at an early stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting tumors using antibodies, nucleotides to secretory protein-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-039447/03
P-PSDB; AAY15136.
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                                       GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle
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                                                                                  CAGGGCATCCGAATTGACTCAGATATCAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATT
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97.53%
97.88%
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Indels:
Gaps:
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(Zsig9) -
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Best Local S. Query Match: DB:
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ABK36007
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                                            US-10-082-502-20 (1-162) x ABK36007
                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                           Score:
                                                                                                                                                                                                                            The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders ce.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. allergic conditions (e.g. neurodegenerative disorders (e.g. hamemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK36232 represent the cDNA sequences of the invention that encode for novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs K, M
                                                                                                         Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merberg D
Clark HF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK36007 standard;
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ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
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Fechtel
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Matches:
Conservative:
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ta K, Graham J
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RESULT 14
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ID AAX97
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XX AX97
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KW Giagn
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XX Homo
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13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
                    Example 28; Page 194-195; 307pp;
                                                         Extended cDNAs encoding secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; diagnostic; gene
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DB; AAY36153.
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gene therapy; chromosome mapping; secretion vector; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment
       expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoletic; chemokinetic; analgesic; haemostat. thrombolytic; antinflammatory; cytostatic; antibacterial; antifunga antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antilicer; osteopathic; neuroprotective; nootropic; antipsoriatic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAY36129-Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.
                                               Human; mouse; chicken; rat; secreted expressed expressed sequence tag; EST; probe; chemotactic immunomodulatory; haematopoletic; chemokinetic;
                                                                                                 Mouse
                                                                                                                          21-AUG-2000
                                                                                                                                                                            AAA43525 standard;
  cerebroprotective;
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799.00
97.58%
96.97%
94.22%
  anticonvulsant;
                                                                                                                                                                            CDNA;
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gene
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Cc chemokinetic; proliferative; immunomodulatory; haematopoletic; cc chemokinetic; antilestic; immunomodulatory; haematopoletic; antilasthmatic; antilasterial; antilucer; osteopathic; antilabetic; cc cytostatic; antilacer; antilucer; osteopathic; antilabetic; cc antiasthmatic; vulnerary; antilucer; osteopathic; neuroprotective; cc anticonvulsant; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the cc identification and isolation of full-length cDNAs and genomic DNA cc molecules which correspond to the SESTs. Proteins encoded by the SESTs care useful in assays for determining biological activity and raising cc antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions cc (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, cc osteoporosis, osteoarthritis, central nervous system disorders (CC Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation cc disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's cc disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; autoimmune disorder; multiple sclerosis; allergic conditional. dependent diabetes; asthma; myeloid cell deficiency; ulc lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
Sequence
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Bowman MR;
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Alignment Scores: 6.37e-82 Length: 592
Pred. No.: 746.50 Matches: 151
Score: 94.48% Conservative: 3
Percent Similarity: 92.64% Mismatches: 8
Best Local Similarity: 92.64% Mismatches: 8
Ouery Match: 88.03% Indels: 3
DB: 648.03% Gaps: 0
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US-10-082-502-20 (1-162) x AAA43525 (1-592)

- Qy 21 GluIleAlaGlnValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro 40

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                                      434 GAGCTC 439
                                                        161 GluLeu 162
                                                                                                                                                                                                             81 HisArgLysAsnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu 100
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432 c 477 g 746 t
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Matches:
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REMARK
COMMENT
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Karlins,E., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA
                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: p Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6014631. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Nation Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-NOV-2000) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General Cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaithersburg, Maryland; Web site: http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Sequencing by: National Institutes of Health
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/tissue_type="Eye, retinoblastoma"
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                                                                                                                                                                                                                        /organism="Homo sapiens"
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                            /codon_start=1
                                                                                note="Vector: porm7"
                                                                                                                'lab_host="DH10B-R"
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Homo sapiens cerebellum cDNA to mRNA, clone_lib:BRACE2
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US-10-082-502-21 (1-162) x BC001027 /protein_id="AAH01027.1"
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VDPKKTIOMGSERINPDGSQSVYEYTVTVPPNKVAHSGFG" 7.57e-17 253.00 100.00% 97.96% 29.87% 9 ဂ (1-824)g Length: Matches: Conservative: Mismatches: Indels: 0 0 0 0

Homo sapiens cDNA FLJ37126 fis, clone BRACE2022693, weakly similar to Transmembrane protein 4. AK094445.1 GI:21753508

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Kawakami,B.,

Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matda,K., Nasauca,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai and Isogai,T human cDNA sequencing project Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Isono, Y.,

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 392-0812, Japan (E-mail:genomics@hri.co.)gp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, annotation: HRI and RAB. 2 (bases 1 to 2378)
Isogai,T. and Yamamoto,J.
Direct Submission /tissue_type="cerebellum"
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GTTCCTTATGCCCGCTCAGAGGCCCACCTCACGGAGTTGCTTGAGGAGATATGTGACCGA
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/db_xref="taxon:10116"
/clone="Ct230-319E6"
/c2934 c 23569 g 23059 t
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83122: contig of 2889 b
83222: gap of unknown 1
86731: contig of 3509 b
86831: gap of unknown 1
86831: gap of unknown 1
8929: contig of 3098 b
90029: gap of unknown 1
93107: contig of 3078 b
93207: gap of unknown 1
93110: contig of 4112 b
97519: gap of unknown 1
97519: gap of unknown 1
101666: contig of 4147 b
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                                                                                                                                                                                                Worley,K.C.

Direct Submission

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 12, 2002 this sequence version replaced gi:18860222.
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-FEB-2002) Human Genome Sequencing Center, Departme of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Project Information
                                                                                                          Center code: BCM
                                                                                                                                        Center: Baylor College of Medicine
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 47 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                  as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 60229 bases at least Q40 Consensus quality: 63959 bases at least Q30 Consensus quality: 66730 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: CH230-319E6
----- Summary Statistics
Sequencing vector: Plasmid;
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of 1423
unknown
of 1449
f unknown
of 1645
                                                                                             length
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REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

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HTG.
Submitted (26-JAN-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
On Jan 26, 2002 this sequence version replaced gi:18201765.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-
30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 207424) Spiegel, L., Preston
                                                                                                                                                                                                                             Submitted (24-FEB-2001) Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratory, 1 Bungtown RcHarbor, NY 11724, USA
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Genomic sequence for Mus musculus, clone RP23-104010, complete
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Kirchoff,K., Kuit,K., Nascimento,L., Zutavern,T., Balija,V.,
Bell,M., Baker,J., Santos,L., Miller,B., Katzenberger,F.,
Beller,S., King,L., Yang,C., Palmer,L., O'Shaughnessy,A. and
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48132. .48165
/note="We belove the assembly to be correct.
is a mononucleotide (T) repeat in which the e
of Ts is unknown. Other subclones in the reg
fewer T than that represented in the assembly
48671 c 49663 g 56477 t
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/clone="RP23-104010"
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                                                                                                                                                                                                                                                                                                                               Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Earlhart, G., Harris, R., Garret, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Frantz, P., Garcia, A., Harris, R., Hawes, A., Hernandez, J., Harris, C., Harris, K., Harris, R., Harris,
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Submitted (15-FEB-2000) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine,
                                                                     Direct Submission
                                                                                                                                                                                                                            Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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                                                                                                                                                              Unpublished
                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                     Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
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Direct Submission
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Sequencing Center, Departmented (24-AUG-2002) Human Genome Sequencing Center, Departmented Rolecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Aug 4, 2002 this sequence version replaced g1:22094227.
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Chemistry: Dye-primer Bodipy: 2% of reads (Chemistry: Dye-terminator Big Dye: 98% of reads (Chemistry: Dye-terminator Big Dye: 98% of reads Assembly program: Phrap; version 0.990329 (Consensus quality: 183845 bases at least Q40 (Consensus quality: 184849 bases at least Q30 (Consensus quality: 185447 bases at least Q20 (Consensus quality: 1850467) (Consensus quality: 1850467) (Consensus quality: 185047) (Consensus
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Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 9 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will 2040: contig of 2040 b 2140: gap of unknown 1 4170: contig of 2030 b 4270: gap of unknown 1 bp in length length length length

/organism="Homo sapiens" /db_xref="taxon:9606" /clone="RP11-183H16" gap of unknown length contig of 31790 bp in lagap of unknown length contig of 35738 bp in lagap of unknown length contig of 64639 bp in lagap of unknown length gap of unknown length contig of 18780 bp in length gap of unknown length contig of 19119 bp in length contig of 4024 of unknown 1g of 5802 Length: Matches: Conservative: Mismatches: 46673 t þ ģ length in length in length 812 others length length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burbaria, J., Bowie, S., Brevan, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Chen, G., Chen, R., Chen, E., Chocker, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Check, J., Chavezo, D., Chavezo, C., Coyle, M.D., Dathorne, S.R., David, R., J., David, K.J., David, K.J., David, R., J., Lander, C., Edgar, D., Edward, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edward, R.C., Enhaj, C., Escotto, M., Earls, T., Ferraguto, D., Edward, R.C., Erist, J., Foster, P., Frantz, P., Edward, S., Huber, J., Hale, S., Hamilton, K., Earls, R., Gaoriell, J.H., Gaoriell, J.H., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Holloway, C., Hollins, B., Hernandez, J., Hollins, R., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Jackson, L.E., Jacobson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Loulseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Nickerson, E., Neckedo, M.P., Meador, M., Mayuen, A., Nguyen, N., Nickerson, E., Neckedo, M.P., Meador, M., Mayuen, N., Nickerson, E., Pup, L.L., Quiles, M., Ren, Y., Reters, L., Peters, L., Peters, L., Peters, L., Peters, L., Shooshtari, M., Sisson, I., Shoek, M., Shoek
                                                                                                                                                     Submitted (24-AUG-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Aug 23, 2002 this sequence version replaced g1:22296903.
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                            Worley, K.C
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Homo sapiens chromosome 12 clone RP11-977G19, WORKING DRAFT
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   Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Sequencing vector: M13;
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 85% of reads
Chemistry: Dye-terminator Big Dye: 85% of reads
Chemistry: Dye-terminator Big Dye: 85% of reads
Consensus quality: 179279 bases at least Q40
Consensus quality: 180581 bases at least Q30
Consensus quality: 181073 bases at least Q20
Estimated insert size: 17258; sum-of-contigs estimation
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17251: contig of 10465 bp in length
17351: gap of unknown length
85894: contig of 68543 bp in length
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Direct Submission
Submitted (11-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 155023)
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Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 3, 2002 this sequence version replaced g1:20335511.
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Center project name: HALV
Center clone name: RP11-348M3
Center clone name: RP11-348M3
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 5% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 14522 bases at least Q40
Consensus quality: 14502 bases at least Q30
Consensus quality: 150442 bases at least Q30
Estimated insert size: 150706; sum-of-contigs estimation
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NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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/db_xref="taxon:9606"
/chromosome="12"
                                                              1. .155023
                                          organism="Homo sapiens"
                                                                                  ocation/Qualifiers
                                                                                                       68406: gap of unknown length
109481: contig of 41075 bg in
109581: gap of unknown length
155023: contig of 45442 bp in
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51104: contig of 8741 bp in length
51204: gap of unknown length
68306: contig of 17102 bp in length
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                                             TGAGAATGGCATATTCCTTTAAATTGTTTGCCATTTGCAGATCTTTGTGACCATGCCCTG
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                                      GATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAG
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Sequence
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                                                                                                                                                                                                                                                                                                                                      Wood, W.L. and Zhang, Z. Secreted and transmembrane polypeptides
                                                                                                                                                                                                                                                                                                                                                Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W. Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Muzayo, M., Adams, C., Addo-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Biankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Belrea, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bayel, N.C., Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Clevel, M.D., Dathorne, S.R., David, R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Deland, C.D., Cox.C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Dauthwatte, K.J., Drager, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earlhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earlhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Becter, J., Frantz, P., Frantz, G., Garza, N., Gill, R., Gorzell, J.H., Guevara, M., Gunaratine, P., Hale, S., Hanilton, K., Frantz, G., Harris, K., Harris, M., Baylas, P., Hawes, A., Holloway, C., Hollins, B., Homsi, F., Howatd, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kully, S., Hanilaney, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Maviliney, E., McLeod, M. P., Meador, M., Morgan, M., Sto
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Yokoyama-Kobayashi,M., Yamaguchi,T., Sekine,S. and Kato,S.
Selection of cDNAs encoding putative type II membrane proteins
the cell surface from a human full-length cDNA bank
Gene 228 (1-2), 161-167 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-JUN-1998) Seishi Kato, Researci Rehabilitation Center for the Disabled, Depare Rehabilitation Engineering; 4-1 Namiki, Toko. 359-8555, Japan (E-mail:seishi@rehab.go.jp, Tel:042-995-3130(ex.2568), Fax:042-995-3132)
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Olsson,P.-A. and Lindholm,D.
Direct Submission
Submitted (13-APR-2001) Neuroscience,
Husargatan 3, Uppsala 75123, Sweden
Location/Qualifiers
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NSAP is a novel saposin-like protein
stimulates neurite outgrowth
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Sequence 309
AX440456
AX440456.1
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="12"

/clone="RP11-764L14"

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153510: gap of unknown 1
155739: contig of 2229 b
155839: gap of unknown 1
158198: contig of 2359 b
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Lodes,M.J., Algate,P.A., Fling,S.P.,
                         type II membrane protein.

Homo sapiens gastric adenocarcinoma cDNA
clone_lib:pXA1-meta-1 clone:HP10390.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                  Homo sapiens
                                                      AB015631
AB015631.1 GI:4586839
                                                                        clone: HP10390.
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/db_xref="taxon:9606"
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Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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Mannion, J., 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 158198)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burter,M., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
                                                                                                                                                                                                                                              SEQUENCE, 5 unordered pic
AC012013
AC012013.18 GI:14717292
HTG; HTGS_PHASE1; HTGS_DF
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158198 bp DNA linear HTG 17-JUL-2001
Homo sapiens chromosome 12 clone RP11-764L14, WORKING DRAFT
                                                                                                                                                                                                              Homo sapiens
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KNYVRVVSRNGESSELDLQGILDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
DKLCSKRTDLCDHALHRSHDELF
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COMMENT

as soon as it is available and be preserved.

the accession number

108230 108330

108229: contig of 108229 bp in length 108329: gap of unknown length 150246: contig of 41917 bp in length

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Submitted (19-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2001 this sequence version replaced gi:14547727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
2 (bases 1 to 158198)
Worley, K.C.
                                                                                                                                                                                                                                                                                                            Center project name: HMKZ

Center clone name: RP11-764L14

Center clone name: RP11-764L14

Sequencing vector: M13; LO8821

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 161278 bases at least Q40

Consensus quality: 170806 bases at least Q30

Consensus quality: 170806 bases at least Q20

Estimated insert size: 163288; sgarose-fp estimation

Pestimated insert size: 163288; sgarose-fp estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

Quality coverage: 5.8x in Q20 bases; sum-of-contigs estimation
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                                                                                                Match:
  \vdash
ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
                                                                                                                                                                                               Scores:
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Der
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: b Collumn: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 9903606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: ang@bcm.tmc.edu
Guntaratne, P.H., García, A.M., Lu, X., Hulyi
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart:
Richards, S., Gibbs, R.A.
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Contact: MGC help desk
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                     /db_xref="LocusID:56530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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S., Martin,
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                                                                                                                                                        Submitted (14-SEP-1999) Biomolecular Informatics, ZymoGenetics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, USA Location/Qualifiers
                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                      O'Hara, P
                                                                                                                                                                                                              Sheppard, P.,
                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                Mus musculus putative secreted
                                                                                                                                                                                                                                                            Sheppard, P., Jelinek, L., Whitmore, T., Blumberg, H., O'Hara, P.
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/db_xref="dbEST:AA049839"
/db_xref="taxon:10090"
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlp
-O-/cgn2_1/USPTO_spool/US10082502/runat_24032003_135059_6547/app_query.fasta_1.1308
-DB-GenEmbl -QFMT-fastap -SUFFIX-rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -STARF-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US10082502_@CGN.1_1_4758 @runat_2403203_135059_6547 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -YGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
-YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Fgapop 6.0 , Fgapext
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                        immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostat thrombolytic; antifinflammatory; cytostatic; antibacterial; antifunga antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antidatebetic; neuroprotective; nootropic; antipsoriatic;
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96.36%
94.55%
92.21%
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                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                      NO:100
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156
                                                                                       antifungal;
                                                                                                                      haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               687
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5 g 5

105 21

ArgargSerGlnaspLeuHisCysGlyalaCysArgalaLeuValaspGluLeuGluTrp |||||||||||| |CGAAGGAGCCAANATCTACACTGTGGANCTTGCAGGGCTCTGGTGGATGAATTAGAGTGG

GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro

6

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US-10-082-502-21 (1-162)
                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                 Alignment
Pred. No.:
                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                Ct tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities depending on the tissues they were isolated from. The activities include: Cc chemotactic; proliferative; immunomodulatory; haematopoletic; cc chemokinetic; analgesic; haemostatic; thrombolytic; antidabetic; cc chemokinetic; antibacterial; antifungal; antiviral; antidabetic; cc chemokinetic; uninerary; antiulcer; osteopathic; neuroprotective; cc antiantmatic; uninerary; antiulcer; osteopathic; neuroprotective; cc nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; cc terropy and in vaccines. The sests can be used for gene cc therapy and in vaccines. The sests are useful as probes for the cc identification and isolation of full-length cDNAs and genomic DNA cc molecules which correspond to the sests. Proteins encoded by the sests can be useful in assays for determining biological activity and raising cc antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions costeoporosis, osteopathritis, central nervous system disorders (condition of the sentral nervous system disorders (condition softener's, Parkinson's, Huntington's disease, stroke), coagulation cd disorders (haemophilla, thrombosis), inflammatory disorders (Crohn's cdisorders (Azabeimer's, bacterial, fungal or viral infections, depression and cc psoriasis. AAA45926 to AAA45931 represent linker variants which are given cc in the exemplification of the breasent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed
such as au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; autolmmune disorder; multiple sclerosis; allergic condition; insulin dependent disbetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parklison's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tags (SESTs)
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA43426 to AAA45925 represent specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                            exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d polynucleotides, and encoded proteins, comprising secreted ed sequence tags (sESTs), useful for treating various disorde autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 228-229; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCoy JM,
Treacy M,
                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US24206
                                                                                                                                                                                       159
                                     3.77e-83
763.50
95.71%
95.09%
90.14%
21
x AAA43525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MR;
                                                                                                                                                                                                                          present invention.
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                                                                                                                                                                                       167
(1-592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from human,
                                                      Mismatches:
Indels:
                                                                                           Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins-Racie
                                                                                                                                                                                       123
                                                                                                                                                                                       Ŧ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse, chicken
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                                   592
155
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and rat
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                                                                                                                                                                                                                                            are given
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RESULT 13 ABK36007

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                US-10-082-502-21 (1-162) x ABK36007
                                                                                                                                Alignment
                                                                                                                                                                                                       The present invention relates to the isolation of novel cDNA sequences CC which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. theodyllia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK36232 represent to company the polynucleotide for novel human accorder of the invention that encode for novel human and the column sequences of the invention that encode for novel human are also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs K,
Merberg D,
Clark HF,
                                                                                                                                                                                                the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2000; 2000US-195605P
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                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; altergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2002
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                                                                                                                                                                                                proteins.
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Fechtel
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                                                                                                                                                              BP; 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatotropic; immunosuppressive;
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                              2.49e-89
815.00
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95.68%
96.22%
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                                                                                                                                                              A; 149 C;
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Agostino MJ, Bowman MR, Spaulding
Howes SH, Resnick RJ, Gulukota K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC.
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(1-657)
                                                                                                                                                                185 G; 146
                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                other;
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155
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lding V, Wong (
ta K, Graham J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , GG;
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ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp

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RESULT 14
AAX97837
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                                                                                                                  04-SEP-1998;
13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
       Example 28; Page 194-195;
                        Extended cDNAs encoding secreted
                                          WPI; 1999-347472/29.
P-PSDB; AAY36153.
                                                                     Bougueleret L,
                                                                                      (GEST )
                                                                                                          10-AUG-1998;
                                                                                                                                                                                                            WO9925825-A2
                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                              Secreted protein; diagnostic; gene
                                                                                                                                                                                                                                                        Secreted
                                                                                                                                                                                                                                                                          Human secreted
                                                                                                                                                                                                                                                                                                              AAX97837;
                                                                                                                                                                                                                                                                                                                                AAX97837 standard; cDNA; 832
                                                                                                                                                                        13-NOV-1998;
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                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                   GAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                       GACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGGAACAGATTGATCCTTCCACC
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                                                                                        GENSET
                                                                                                                                                                                                                                               gene therapy; chromosome
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                         97US-0069957.
98US-0074121.
98US-0081563.
98US-0096116.
                                                                                                                                              98US-0099273.
97US-0066677.
                                                                                                                                                                                                                                                                         protein encoding cDNA
                                                                                                                                                                        98WO-IB01862
                                                                     Duclert
                                                                                                                                                                                                                                                        human; cytostatic;
                                                                     P
       307pp; English
                                                                      Dumas
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                                                                      Milne Edwards
                                                                                                                                                                                                                                              mapping; secretion vector; ss.
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SSSS

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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AAX97884
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Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment
                                                                                                      Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic; diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
                                                                                                                                                                                                                                                 1083
                                                                                                                                        Human secreted
                                                                                                                                                                                                      AAX97884 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO polypeptides can be used to transgenic or knock out animals
04-SEP-1998;
                     13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.:
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                                                                                                                                                                                                                                                                                         GluLeu
                                                                                                                                                                                                                                                                                                                                   GAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                   HisargLysasnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGGAACAGATTGATCCTTCCACC
                                                                                                                                                                                                                                                                     162
                                                                                                                                                                                                                                                 1088
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                     98WO-IB01862
                                                                                                                                      protein encoding
98US-0099273
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830.00
98.77%
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17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAX56129-X36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 272; 307pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 714
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                                                                                                                                    GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
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                             GluLeu 162
                                                                                                                                                                                          HisargLysasnTyrValargValValSerArgAsnGlyGluSerSerGluLeuAspLeu
                                                                                                                                                                                                                                    LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr
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         GAGCTA
                                                              AspLysLeuCysSerLysArgThrAspLeuCysAspH1sAlaLeuH1sArgSerH1sAsp
                                                                                                                                                                               CATCGCAAGAACTACGTGCGTAGTGGGCCCGGAATGGAGAATCCAGTGAACTGGACCTA
                                                                                                                                                                                                                         CTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGAACAGATTGATCCTTCCACC
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                                                                                                                                                                                                                                                                                                              GAMATTGCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCA
                                                    GACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATGAT
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         578
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97US-0069957.
98US-0074121.
98US-0081563.
98US-0096116.
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                                           Human cDNA sequence encoding for PRO4426 polypeptide.
                                                                                                                                                                                            1053
    breast;
             Human secretory and
                                                                                                                                  AAS21330 standard;
                                                                           24-OCT-2001
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                                                                        (first entry)
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   cervical;
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830.00
98.77%
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                transmembrane; PRO; mammalian;
 tumour necrosis
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factor-alpha; TNF-alpha;
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01-DEC-2000;
                                                            07-JUN-2001.
                                                                                                                                                                                                                                 cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
2000WO-US32678
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01-DEC-1999

01-DEC-1999

02-DEC-1999

02-DEC-1999

02-DEC-1999

03-DEC-1999

16-DEC-1999

20-DEC-1999

20-DEC-1999

20-DEC-1999

30-DEC-1999

30-DEC-1999

16-JAN-2000

11-FEB-2000

11-FEB-2000

18-FEB-2000
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24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
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2000WO-US05004
2000WO-US05004
2000WO-US05001
2000WO-US07537
2000WO-US07537
2000WO-US08439
2000WO-US13705
2000WO-US14941
2000WO-US14941
2000WO-US15264
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99WO-US31243.
2000WO-US00277.
2000WO-US00376.
2000WO-US03565.
2000WO-US03441.
2000WO-US04341.
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99WO-US30095.
99WO-US30911.
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(GETH) GENENTECH INC.

Gerritsen ME, Goddard Smith V, Stewart "" Deforge L, Desnoyers L, A, Godowski PJ, Gurney *I* Tumas D, Watanabe CK, W Wood WI, Filvaroff E, L, Sherwood S; 22 Ξ

P-PSDB; WPI; 2001-408281/43. DB; AAU12258.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -

Claim 3; Fig 173; 813pp; English.

В Š 밁 õ В ð 밁 Š 밁 Ş В δ 밁 S 밁 Š 밁 Ş

CC PRO polypeptides. The PRO polypeptides are useful to detect other CPRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. CC come of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC cortilage, the proliferentiation of chondrocytes, the proliferation or cortilage, the proliferation or alpha equipment of the release of proteoglycans from cartilage, the proliferation of inner ear urricular supporting cells or cof T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by completed in binding interactions. The polynucleotides encoding

WO200190154-A2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and for treating ovarian cancer in a patient. An antigen presenting cell that expresses the sequences is useful for treating ovarian cancer by incubating CD4+ and/or CD8+ T cells isolated from a patient. The T cells can then be proliferated and administered to the patient to inhibit the development of cancer. The DNA sequences are useful as probes or primers for nucleic acid hybridisation, to direct expression of a polypeptide in appropriate host cells. Detecting the presence of a cancer in a patient involves obtaining a biological sample from the patient, contacting the mount of protein that binds to the agent that binds to the protein, detecting the protein to a predetermined cut-off value and determining the presence of cancer. Sequences ABK09464-ABK09802 represent PCR primers and cDNA molecules encoding ovarian tumour proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide encoding polypeptide comprising overland tumour protein, useful for detection, diagnosis and human overlan cancer
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13-JUN-2000; 2000US-213673P.
21-JUN-2000; 2000US-213673P.
03-AUG-2000; 2000US-223288P.
01-MAR-2001; 2001US-272790P.
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sequences of the invention are useful for
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                                              81
                                                                                      GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                        ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
CATCGCAAGAACTACGT
                             H1sArgLysAsnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu
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01-JUL-1997;
01-JUL-1997;
                 The invention relates to nucleic acid sequences (AAX22111 to AAX22134) encoding human secreted proteins (AAV01135 to AAV01158). The secreted protein gene sequences are deposited with the ATCC under deposit number ATCC 209118. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; gene therapy; protein therapy; tissue; cance; tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AII developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; schizophrenia; immunological disorder; mood disorder; immune deficiency disease; respiratory disorder; arthritis; skeletal; haematopoietic disorder; neural; osteoporosis; metabolic disorders; cardiovascular; endocrine; gastrointestinal; asthma; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, immune deficiency diseases or blood
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                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 117;
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P-PSDB; AAY01136, AAY01162, AAY01163.
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                                                                                 Antibody preparation by inoculation of an animal with a vector expressing a fusion protein of an antigen on the C-terminal side transmembrane domain for use as drugs, diagnostic reagents and
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24-AUG-2000;
                        Example;
                                                                                                                                   Antibody
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DB; ABB09717.
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                              Human; ovarian tumour protein; cancer; cytostatic;
gene therapy; CD4+ T cell; CD8+ T cell; PCR primer
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      Expressed sequence tag; EST; human; cancer; anti-neoplastic; cytotoxic T lymphocyte; chemotherapy; cytostatic; chromosome 12; transmembrane protein 4; gene; ss.
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CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGG GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro US-10-082-502-21 (1-162) x ABK52765

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                                                                                                                         Sequence 814
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/product= "Transmembrane protein
                                                                                                                       210 A; 194 C;
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                                                                                                                                                                                                                                                    protein-9, zsig9 that arises due to alternative splicing, allelic variation or silent mutations that result in amino acid changes. This sequence is mapped to the human chromosome 12q15 region. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to Zsig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to Zsig9 and it may be radio-labelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of Zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding Zsig9. The Zsig9 sequence facilitates improved diagnostic and therapeutic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overexpression; antagonist; antibody; antisense nucleotide; tumour; treatment; receptor; radio-label; fusion; polypeptide toxin; technique down-regulation; probe; diagnostic; therapeutic; cancer; brain; liver; detection; stomach; lymphoma; alternative splicing; allelic variation; silent mutation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting tumors using antibodies, antagonists nucleotides to secretory protein-9 (2s1g9) -
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/note= "Overexpressed in tumours"
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                  Claim 4; Page 106-107; 114pp;
                                               Human proteins with proliferation and di
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ds.
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e.g. cancer or
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sequence represents

the human cDNA clone HP10390

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19-MAY-1998;
17-JUN-1998;
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03-JUL-1997;
03-JUL-1997;
This cDNA clone encodes human secretory peptide-9, or Zsig9, wariant (see AAW88474). Zsig9 (see also AAW88469) is overexpr. human brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors. Thus, Zsig can be used as an indicator for cancer. Zsig9 cDNA was discovered in a placenta clone from a full-term pregnancy cDNA library which contained a
                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                           Claim
                                                                                                        New mammalian secretory peptide-9 (Zsig9) - enhancer for placenta, liver and heart, and
                                                                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag (see AAX06971). The invention provides polynucleotides (see AAX06968-70) encoding Zsig9 polypeptides (see AAX08968-77) including mature polypeptides, other processed forms, variants and mouse orthologues. The Zsig9 gene, or probes derived from it, can be used to determine if Zsig9 is present on chromosome 12, and if a mutation has occurred. Antibodies raised against zsig9 can be used as diagnostic agents to determine the presence of Zsig9 can be used as diagnostic agents to determine the presence of the Xsig9, and thus the presence of cancer. They can also be labelled with radioisotopes or fused with toxins and used to treat tumours which oversyress Zsig9. Antisense nucleotides derived from Zsig9 cDNA can also be used to inhibit the growth of tumour cells. Zsig9 proteins can be used to enhance the growth or development of the
                                                                                                   AAZ08293 standard;
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                                                                                                                                                                                               GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle
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                                                                                                                                                                                                                                                                                                                                                           HisArgLysAsnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu
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                                                                                                                                                                                                                                               GTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAA
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                                                                                                                                                                                                                                                                                                                                               CATCGCAAGAACTACGTACGTGGGGGGGGGGAATGGAGAATCCAGTGAACTGGACCTA
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Secretory protein-9; Human Zsig9; chromosome 12q15 region; variant;

Human Zsig9 gene encoding secretory protein variant-4.

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assay reagent; diagnostic marker; primer;
agonist; antagonist; ligand; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present DNA sequence is an ortholog encoding the secretory protein-9, 2sig9 derived from mouse. It is overexpressed in tumours. Antagonists, antibodies and antisense nucleotides to Zsig9 are useful for detecting and treating tumours. The antagonist may be an antibody or receptor to Zsig9 and it may be radio-labelled or fused to a polypeptide toxin. It can be used for down regulating the overexpression of Zsig9. The gene sequence can be used as nucleic acid probes to detect RNA encoding Zsig9. The Zsig9 sequence facilitates improved diagnostic and therappettic techniques for detecting and treating cancers, especially of the brain, liver, stomach, lymphoma etc., at an early stage.
                    HP10390; transmembrane domain; stomach cancer cell; antibody;
                                              Human transmembrane
                                                                                                                   AA238326 standard;
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                                            HP10390 coding sequence
 probe; antisense; ds.
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                                                                                                                                                                                                                                                                                                                                                             This sequence represents the coding sequence of human cDNA clone HP10390 which encodes a 20 KD protein with one putative transmembrane domain in the N-terminus. The cDNA was isolated from a human stomach cancer cell line cDNA library. The protein has no homology with any known protein. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins with transmembrane domains, proliferation and differentiation, useful inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kato
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(PROT-)
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          LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr
                                                 GATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAG
                                                              AspGlySerGlnSerValValGluValProTyrAlaArgSerGluAlaHisLeuThrGlu
                                                                                                     GAAATTGCCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCA
                                                                                                                  GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
                                                                                                                                                       CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGG
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CTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGGAACAGATTGATCCTTCCACC
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)B; AAY52391.
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HisargLysasnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu

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                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                          This cDNA clone encodes novel mouse secretory peptide-9, or Zsig9 (see AAW88476), an orthologue of novel human Zsig9 (see AAW88469). Human Zsig9 is overexpressed in a number of tumours including brain, liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma tumors, and thus can be used as an indicator for cancer. The invention provides polynucleotides (see AAW86968-70) encoding Zsig9 polypeptides (see AAW88469-77) including mature polypeptides, other processed forms, variants and the mouse orthologues. The Zsig9 gene, or probes derived from it, can be used to determine if Zsig9 is present on chromosome 10, and if a mutation has occurred. Antibodies raised against Zsig9 can be used as diagnostic agents to determine the presence of Zsig9, and thus the presence of cancer. They can also be labelled with radiolsotopes or fused with toxins and used to treat tumours which overexpress Zsig9. Antisense nucleotides derived from Zsig9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-1997;
19-MAY-1998;
19-MAY-1998;
17-JUN-1998;
                                                                                                                                                                                                                                                                                                 cDNA can also be used to inhibit the growth of tumour cells. Zsig9 proteins can be used to enhance the growth or development of the placenta, heart or liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 75-77; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian secretory peptide-9 (Zsig9) - enhancer for placenta, liver and heart, and
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03-JUL-1997;
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                                                            GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro
                                                                                                              ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
AspGlySerGlnSerValValGluValProTyrAlaArgSerGluAlaHisLeuThrGlu
                                                CGAAGGAGCCAAGATCTACACTGTGGAGCTTGCAGGGCTCTGGTGGATGAATTAGAGTGG
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98US-0085983.
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97US-0051704.
97US-0888088.
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 AAZ08294
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Disclosure; Page 37-38; 45pp; English.
                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                        antibody; antisense nucleotide; tumour; treatment; receptor; radio-label; polypeptide toxin; down-regulation; disgnostic; therapeutic; probe; cancer; brain; liver; detection; stomachlymphoma; ds.
                                                                                                                                                                                                                                                                                                                                          07-FEB-2000
             Detecting tumors using antibodies, antagonists nucleotides to secretory protein-9 (Zsig9)
                                        WPI; 2000-039447/03.
P-PSDB; AAY15136.
                                                                                                                                                                                  mat_peptide
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                                                                 Moore
                                                                                                 19-MAY-1998;
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                                                                                                                                  25-NOV-1999
                                                                                                                                                  WO9960405-A1
                                                                                                                                                                                                                                                                                                         Secretory protein-9; mouse 2s1g9; ortholog; overexpression; antagonist;
                                                                                                                                                                                                                                                                                                                        Mouse ortholog gene encoding Zsig9 secretory protein.
                                                                                (ZYMO ) ZYMOGENETICS
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418..903
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/product- "Mouse Zsig9 secretory protein"
/note- "Overexpressed in tumours"
358.417
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                                                                                                                                                                 /label= Mature_Zsig9_protein_variant-4
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-MODEL-frame+p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/US10082502/runat_24032003_135058_6538/app_query.fasta_1.1308
-DB-N_Geneseq_101002 -QFMT-fastap -SUFFIX-rng -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-blts -START=1 -END-1 -MATRIX-blosum62 -TRANS-human40.cd1
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OOTFMT-pco -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US10082502_eGCN_1_1_741_erunat_24032003_135058_6538 -NCPU-6 -ICPU-3
-NO_MAND -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XOAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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1 RRSQDLHCGACRALVDELEW.....LCSKRTDLCDHALHRSHDEL 162
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	AAZ10655	20	718	29.9	253	23
Zsig9 gene	AAZ08284	21	649	٠	253	22
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secrete	AAX97883	20	649	٠	253	20
breast	AAL26689	22	1160	٠	380	19
breast	AAL07882	22	595	44.9	380	18
breast	AAL18023	22	558		380	17
breast ca	AAL25628	22	484		380	16
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ALIGNMENTS

RESULT 1 AAX06970 AAX06970 standard; cDNA; 1069 BP

AAX06970;

10-MAY-1999 (first entry)

Mouse secretory peptide-9 (Zsig9) orthologue cDNA.

Secretory peptide-9; Zsig9; orthologue; mouse; tumour marker; cancer; therapy; diagnosis; growth enhancer; ss.

Mus sp.

CDS Location/Qualifiers 358..906 /*tag-.

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US-10-082-502-21 (1-162) x US-09-139-491-38 (1-4131)
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Best Local Similarity:
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APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6015677and, Greta E.
REGISTRATION NUMBER: 27866/30822
REFERENCE/DOCKET NUMBER: 2786
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STRANDEDNESS: single
TOPOLOGY: 14--
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPARTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,491
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LENGTH: 4131 base pair
841 CTGCAACAGGAGACCCAGGCATCCCGCTGCTGCTGCTGCTGGTATCCGAGGACAAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 IleAsnProAspGlySerGlnSerValValGlu------ 48
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                                                                   89 ValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp 108
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CLASSIFICATION:
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                                                                                                                                                                                                                          MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgVal 88
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                    146 LysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAspGluLeu 162 ::: ||||:::: |||
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                                                                                                                                                                                             129 IleGluPhe-----PheSerArgGluAlaAspAsnValLysAspLysLeu----- 143
                                                                                                                                                                                                                                    -----CysSer 145
                                                                                                                                                          ATCAGCTTTCCGTTGACCACAGGACGCCTGGGCCAAGTGGTGGAAGACAAGAAGTCTATC 1005
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Search completed: March 31, 2003, 04:26:21 Job time: 45.3198 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38,
                                                                                        TELEFAX: (312) 984-970
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pair
                                                                                                                                                REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: No. 5800987and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1006 CAGCTGAAAGATCTCACCTCCGAGGATATGCAACAGCTGCAAAGCATGTTGGGCTGTGAG 1065
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 LysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAspGluLeu 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                  FILING DATE: US 07/688,356
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
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                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleGluPhe-----PheSerArgGluAlaAspAsnValLysAspLysLeu-----
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5800987
                                 nucleic acid
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                                                    4131 base pairs
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                                                                                                                                   (312) 984-9740
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                   single
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                                                                                                                                                                                                                                                                                                                       08/297,494
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                                                                                                                                                                                         27866/30822
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US-09-139-491-38
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Best Local Similarity:
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                                                                                                                                                                                                 Sequence 38, Application US/09139491
Patent NO. 6015677
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
                                                                                                                                                                                APPLICANT:
                                                                                                     APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: FEATURE:
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                                 ADDRESSEE: Marshall ADDRESSEE: Bicknell
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                                                                                                                                                                                                                                                                                                                                                                                                           CAGCTGAAAGATCTCACCTCCGAGGATATGCAACAGCTGCAAAGCATGTTGGGCTGTGAG
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Street
               Two First National Plaza, 20 South Clark
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                                                Marshall, O'Toole, Gerstein, Murray
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Conservative:
Mismatches:
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143 945 744

684

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TELEPHONE:

(312)

984-9740

(312) 346-5750

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RESULT 13
US-08-455-526-38
; Sequence 38, Application U
; Patent No. 5789553
; GENERAL INFORMATION:
APPLICANT: Beavo, Jose
; APPLICANT: Bentley, Ke
; APPLICANT: Charbonneau
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                    GTGCAGGCCATGCTCTGTGTCCCTGTCATCAGCCGGGCCACTGACCAGGTC 1116
                                                                                                                                                                 LysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAspGluLeu
                                                                                                                                                                                             CAGCTGAAAGATCTCACCTCCGAGGATATGCAACAGCTGCCAAAGCATGTTGGGCTGTGAG 1065
                                                                                                                                                                                                                                                                                                                                                                                                       ValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp 108
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 Bentley, Kelley
Charbonneau, Harry
                                Beavo, Joseph A.
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148..2910
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                                                                           US/08455526
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Conservative:
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US-10-082-502-21 (1-162) x US-08-455-526-38 (1-4131)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/297,494

FILING DATE: 29-AUG-1994

APPLICATION NUMBER: US 07/688,356

FILING DATE: 04-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: NO. 5789553and, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30822

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF IN
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 745
                                                                       685
                                                                                                                                        625 GAGAAGCATACCCTGGTGGCCCTGAAAAGGGTGCAGGCCTTGCAGCAGCGCGAGTCCAGC 684
                                                                                                                                                                                                             574 GTGCACTGTGT-----CAGCTGAGTGACAATGAGGAGTGGAGCCTGCAAGCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/455,526 FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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COMPUTER: II
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two First National Plaza, STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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GTCGCATACACAAACCAAGACCGAAAGATCCTGCAGCTTTGCGGGGGAGCTCTACGAC---
                               ValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluValCysAspArg
                                                                    GTGGCCCCGGAAGCGACCCAGAATCCTCCGGAGGAGGCAGCGGGAGACCAGAAGGGTGGG
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VENTION: DNA Encoding Mammalian
VENTION: Phosphodiesterases
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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312) 984-9740
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76.00
37.06%
18.78%
8.97%
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Matches:
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GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: BentLey, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
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Best Local Similarity:
Query Match:
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; LOCATION:
US-08-297-510-38
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US-08-297-510-38
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SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPANE: (312) 346-5750
TELEPAN: (312) 384-9740
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
FILING DATE:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA
                                                                         574 GTGCACTGTGGT------CAGCTGAGTGACAATGAGGAGTGGAGCCTGCAAGCTGTG 624
625 GAGAAGCATACCCTGGTGGCCCTGAAAAGGGTGCAGGCCTTGCAGCAGCGCGAGTCCAGC 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two First National Plaza, 20 South Clark STREET: Street CITY: Chicago STATE: Illinois COUNTRY: USA
                                       26 AspProLys-----
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ADDRESSEE: Bicknell
                                                                                                6 LeuH1SCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaArgVal 25
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76.00
37.06%
18.78%
8.97%
                                     ------LysThrIleGlnMetGlySerPheArg 37
                                                                                                                                                                                                                                                                Length:
Matches:
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Indels:
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6/30822	REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 27866, TELECOMMUNICATION INFORMATION:	
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Ā	APPLICATION NUMBER: 08/297,494 FILING DATE:	
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,532	ATION NUMBER:	
.0, Version #1.25		
So.	COMPUTER: IBM PC compatible COMPATING SYSTEM: BC-DOS MS-TX	
	READABL	
	COUNTRY: USA	
	Chicago	• • •
Plaza, 20 South Clark	Two First National Street	
Gerstein, Murray &	ADDRESSEE: Marshall, O'Toole, ADDRESSEE: Bicknell	
	NUMBER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS:	
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	APPLICANT: Bentley, Cosepi A APPLICANT: Bentley, Kelley APPLICANT: Charbonnes: Harry	
2	8 Applicat: 76752 RMATION:	~ ~ · · g
ATCAGCCGGGCCACTGACCAGGTC 1116	1066 GTGCAGGCCATGC	B B
LeuHisArgSerHisAspGluLeu 162	146	Ş,
CAGCTGAAAGATCTCACCTCCGAGGATATGCAACAGCTGCAAAGCATGTTGGGCTGTGAG 10	1006	뫄
CysSer 1	144	õ
ATCAGCTTTCCGTTGACCACAGGACGCCTGGGCCAAGTGGTGGAAGACAAGAAGTCTATC 10	946	Вb
ysasp	129 IleGluPhe	δÃ
-CTTCAGCTCCTGCAAGGTCATTGGAGATAAAGTACTGGAGGAAGAG 94	898	DЬ
rGlyThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeu 12	109 Ilese	δō
CTGCAACAGGAGACCCAGGCATCCCGGCTGCTGCTGCTGCTGGTATCCGAGGACAAT 89	841	밁
leArgIleAspSe	89 ValSer	γQ
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ValProTyrAlaArgSerGluAlaH1sLeuThrGluLeuLeuGluGluValCysAspArg 68 GTCGCATACACAAACCAAGACCGAAAGATCCTGCAGCTTTGCGGGGAGCTCTACGAC 80	49 V 745 G	B 8
GTGGCCCCGGAAGCGACCCAGAATCCTCCGGAGGAGGCAGCGGGAGACCAGAAGGGTGGG 744	685	밁
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 558U//1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonneaburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1066 GTGCAGGCCATGCTCTGTGTCCCTGTCATCAGCCGGGCCACTGACCAGGTC
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                                                                                                                                                           CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
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                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                       STREET: Two First National Plaza,
                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAspGluLeu ::: |||| | ||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCTGAAAGATCTCACCTCCGAGGATATGCAACAGCTGCAAAGCATGTTGGGCTGTGAG 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCAACAGGAGACCCAGGCATCCCGCTGCTGCTGCTGCTGGTATCCGAGGACAAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetLysGluTyrGlyGluGlnTleAspProSerThrHisArgLysAsnTyrValArgVal 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGCATACACAAACCAAGACCGAAAGATCCTGCAGCTTTGCGGGGAGCTCTACGAC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp 108
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5. 5580771
      ARE: Patentin Release #1.0, APPLICATION DATA:
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                                                                                                                                             USA
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Indels:
                        Version #1.25
                                                                                                                                                                                                                           20 South Clark
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-297-494-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEPAX: (312) 984-9740
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5580771and, Gr
                                      1006 CAGCTGAAAGATCTCACCTCCGAGGATATGCAACAGCTGCAAAGCATGTTGGGCTGTGAG 1065
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APPLICATION NUMBER:
                                                                                                                      946
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                                                                                                                                                                                                                                                                                  841
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146 LysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAspGluLeu 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                            745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625 GAGAAGCATACCCTGGTGGCCCTGAAAAGGGTGCAGGCCTTGCAGCAGCGCGAGTCCAGC 68
                                                                                                                                                                                                                                                                                                                         89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaArgVal::::||||||||| ::: ||||
                                                                                                                    ATCAGCTTTCCGTTGACCACAGGACGCCTGGGCCAAGTGGTGGAAGACAAGACTCTATC 1005
                                                                                                                                                                                                -----CTTCAGCTCTCCTGCAAGGTCATTGGAGATAAAGTACTGGAGGAAGAG
                                                                                                                                                                                                                                     IleSerGlyThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeu 128
                                                                                                                                                                                                                                                                                CTGCAACAGGAGACCCAGGCATCCCGCTGCTGCTGCTGCTGCTATCCGAGGACAAT---
                                                                                                                                                                                                                                                                                                                   ValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAsp 108
                                                                                                                                                                                                                                                                                                                                                            MetLysGluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGCATACACAAACCAAGACCGAAAGATCCTGCAGCTTTGCGGGGAGCTCTACGAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluValCysAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGCCCCGGAAGCGACCCAGAATCCTCCGGAGGAGGCAGCGGGAGACCAGAAGGGTGGG
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                                                                                                                                                       IleGluPhe-----PheSerArgGluAlaAspAsnValLysAspLysLeu-----
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCLI Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILTUS DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3752 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettu
COMPUTER: HP Vectra
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PRIOR APPLICATION DATA:
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872 GAACTTGAAAAAACTTCTTGACAGCCTTGATCCTGAAGGTAAGACTCAGGATGAATTAGAT 931
                                                                            761 CTTCTTGCTGGTGCG------GATCCTGATGATGGCACAGAAGTTATAGAAGCTAAA 811
                                                                                                                                                                                                                                    701 ATTTCTACTTTGGAACAAGAAGTTGCTACTGCTCAACATCAAGTAGATAATTTGAAAAAA 760
                                                                                                               51 TyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluValCysAspArgMetLys 70
                                                                                                                                                                                               31 IleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSerValValGluValPro 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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                                     71 GluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgValValSer 90
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                                                                                                                                                                                                                                                             ValAspGluLeuGluTrpGluIleAla-----ArgValAspProLysLysThr 30
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5. 6420135
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9410 Key West Avenue
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RESULT 9
US-07-872-644-38
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   Percent Similarity:
                                Pred. No.:
                                              Alignment Scores:
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                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 07/688,356
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5389527and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
                                                                                                                           FEATURE:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS LENGTH: 4131 base pai:
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                         MOLECULE TYPE:
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                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US
FILING DATE: 19920420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
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                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: Lir
                                                                                                                                                                                TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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Sonnenburg, William K.
SONNENDIN: DNA Encoding Mammalian
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Matches:
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Vaccines

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RESULT 7
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; LOCATION:
US-08-971-988-1
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Best Local Similarity:
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Sequence 159, Application US/08961083 Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
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INFORMATION FOR SEQ ID NO:
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LENGTH: 6519 base pair
                                                                                                                 5145 GAGATA 5150
                                                                                                                                                                                                                                                5043 CCAAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              4863 GTCCGAATCATGCCCTCAAGTCTGGATGATAGAAGAGGCAGCCGCCCCCGGTCCATGGTG
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ORIGINAL SOURCE:
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HYPOTHETICAL:
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                                                                                                                                                161 GluLeu 162
                                                                                                                                                                                                             141 AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAsp 160
                                                                                                                                                                                                                                                                   122 GluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnVal---Lys
                                                                                                                                                                                                                                                                                                                                                                                                            87 ArgValValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIle---ArgIle
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                              AspSerAspIleSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluGlnIleAspProSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACGAGAGGATGGAGGCCTGTTTCAAACAGCTGAAGGAAAAGGTGGAGAAAGAGTACGGC
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DB:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: DISKette.
COMPUTER: HP Vectra 4/
OPERATING SYSTEM: MSDG
SOFTWARE: ASCII Text
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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. APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                              51
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                                                                                                                                                                                                                                                                                                                                                                                                                15 ValAspGluLeuGluTrpGluIleAla------ArgValAspProLysLysThr
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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ATATTACTTGGAGGGGCTGATNCTGAAGATGATACTGCTGCTCCTTCAAAATAAATTAGCT
                                PhePheSerArgGluAlaAspAsn----
                                                                                             GlyThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeuIleGlu 130
                                                                                                                               AAAGAAGCAGAAGAAGCTGAGTTGGATAAAAAAGCTGATGAACTTCAAAATAAAGTTGCT
                                                                                                                                                             ArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArgIleAspSerAspIleSer 110
                                                                                                                                                                                             GAACTTGAAAAACTTCTTGACAGCCTTGATCCTGAAGGTAAGACTCAGGATGAATTAGAT 805
                                                                                                                                                                                                                          GluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgValValSer 90
                                                                                                                                                                                                                                                            TyralaargSerGlualaHisLeuThrGluLeuLeuGluGluValCysaspargMetLys 70
                                                                                                                                                                                                                                                                                                                             CTTCTTGCTGGTGCG-----GATCCTGATGATGGCACAGAAGTTATAGAAGCTAAA 685
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                             US-10-082-502-21 (1-162) x US-08-588-985-1 (1-6519)
                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                         Alignment Scores:
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Patent No. 5777094
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                     FEATURE:
NAME/KEY:
LOCATION:
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APPLICATION DATA:

APPLICATION NOTA:
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LENGTH: 6519 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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SOFTWARE: Wordper
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                                                                                                                                                                                                                                                                                                                                                          LENGTH: 6519 base pairs
TYPE: nucleic acid
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6 LeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaArgVal 25
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08971988 Patent No. 5786461
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Michiy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4660 TTACAGACCGGTACCTGCAGGAGCACCCTGAGGCCCCATGAAA----
                             REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                    FILING DATE: 17-NOV-CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                             SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5085
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                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5145
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5043 CCAAAG------GAAAATGCACTCCAGGTCCCAGGACAAGCTGGACAAG 5084
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Michiyuki MATSUDA et al.
TITLE OF INVENTION: cDNA OF DOCK180 GENE AND DOCK180 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
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                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: Wordper
                                                                                                                                                                                                                                                                                                                             STREET: 805 Fift
CITY: Washington
STATE: D.C.
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                                                                                                        APPLICATION NUMBER: FILING DATE:
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             TELEPHONE:
                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspProLysLysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSer
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Street, N.W.,
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; NUMBER OF SEQ ID NOS:
; SOFTWARE: FastSEQ for
; SEQ ID NO 14
; LENGTH: 915
; TYPE: DNA
; ORGANISM: MOUSE
US-09-724-864-14
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                                                         Sequence 10, Application US/08257073
Patent No. 5766597
GENERAL IMFORMATION:
APPLICANT: Paolett1, Enzo
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APPLICANT: Watson, James G.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
APPLICANT: de Tais:
APPLICANT: Tine, JO
TITLE OF INVENTION:
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                                                                                                                                                                                                  572 AGAGAAGAGCTT 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 CTGCGCTGCGATGCCTGCCGGGCTGTGGCCTTCCAGATGGGGCAACGTCTGGCGAAAGCA 217
                                                                                                                                                                                                                                       159 HisAspGluLeu 162
                                                                                                                                                                                                                                                                                                                                                            452 TACCTGGGTGAGTTTGGAGAGGACCAGATCTATGAAGCCTACCGCCAAGGCCAAGCGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 CAGATGAAGCGTCTCACGGGCCCAGGACTTAGCAAGGGGCCAGAG------CCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 GAGGCTAAATCTCAC-----GGA 250
                                                                                                                                                                                                                                                                                                                                                                                               120 IleValGluGluTyr---GluAspGluLeuIleGluPhePheSerArgGluAlaAspAsn 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 TyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeuGlnGlyIleArg 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 ValValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 AspProLysLysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSer 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaArgVal 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGAGGCGCTGCTGTGGGGGCACCCATGGGCCCTGCTCACAGGAGATCCTGGCCCAG
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                  Paoletti, Enzo
de Taisne, Charles
Tine, John A.
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MALARIA RECOMBINANT POXVIRUS VACCINE
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 840-071
TELEX: 425066 CURTNS
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                      1432 GATAATAAGGAAAGAAAATATTCATTAATAACATTAAAAAAACAAATTGATTTAGAAGAA 1491
                                                                                                                  1372 TCATATGGTGATTTAATGAATCCTGATACTAAAGAAAAAATTAATGAAAAAATTATTACA 1431
                                                                                                                                                                                                1312 GTATATCCTTTACCACTCACTGATATTCATAATTCATTAGCTGCAGATAATGATAAAAAT 1371
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103 IleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIleValGlu 122
                                                                             91
                                                                                                                                                                                                                                     56 AlaHis-----LeuThrGluLeuLeuGluGluValCys-----AspArgMetLys 70
                                                                                                                                                                                                                                                                                                                                                                              16 AspGluLeuGluTrpGluIleAlaArgValAspProLysLysThrIleGlnMetGlySer
                                                                                                                                                       71 GluTyrGlyGluGlnIleAspProSerThrHisArgLysAsnTyrValArgValValSer
                                                                                                                                                                                                                                                                                                                36 PheArgIleAsnProAspGlySerGlnSerValValGluValProTyrAlaArgSerGlu 55
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STRANDEDNESS:
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O Fifth Avenue, 25th Floor
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SEQUENCE CHARACTERISTICS: LENGTH: 744 base pairs

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; LOCATION:
US-09-163-285-3
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                             Sequence 1, Application US/09163285 Patent No. 6204013
                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Khodad
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AGACACGTGCCTTACAGCGTTTCAGAGACAAGGCCTGGAAGAGGCCCTTAGAGAATTTATGT 282
                                                                   COUNTRY: USA
ZIP: 02109
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 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GlyThrLeuLysPheAlaCysGluSerIleValGluGluTyrGluAspGluLeuIle 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspArgMetLysGluTyrGlyGluGlnIleAspProSerThrHis-----ArgLysAsn 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTG-----GATACAGGCAAGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                  Glu---PhePheSerArgGluAlaAspAsnValLysAspLysLeuCys 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGGGGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnGlyIleArgIleAspSerAspIleSer---- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCGGATCCTGGACTAT-------AGTGTTCACGCTGAGCGCAAGGGC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluValCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProLysLysThrIleGlnMetGlySerPheArgIleAsnProAspGlySerGlnSerVal 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaArgValAsp---
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                                                                                                                      Boston
                                                                                                      Massachusetts
                                                                                                                                      E: LAHIVE & COCKFIELD, 28 State Street
                                                                                                                                                                                                                                             Khodadoust, Mehran
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PC-DOS/MS-DOS
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                                                                                                                                                                                                                        NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-082-502-21 (1-162) x US-09-163-285-1 (1-1512)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: June 24, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/163,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                  407
                                                                                             130 Glu---PhePheSerArgGluAlaAspAsnValLysAspLysLeuCys 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1512 base pairs TYPE: nucleic.acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: MNI-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mandragouras, Amy E REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CysGlyAlaCysArgAlaLeuValAspGluLeuGluTrpGluIleAlaArgValAsp---
                                                            GACTGGTACTTCCACCATCAGGAGCAGCCCCTACAAAATTTTCTCTGT
                                                                                                                                        GTCACATACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGA 628
                                                                                                                                                                                                                           AAGGGGGTGAAGGTGGATCTGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAG 568
                                                                                                                                                                                                                                                                      GlnGlyIleArgIleAspSerAspIleSer------
                                                                                                                                                                                                                                                                                                           TCACTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAG 508
                                                                                                                                                                                                                                                                                                                                                    TyrValArgValValSerArgAsnGlyGluSer-----SerGluLeuAspLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                       AspArgMetLysGluTyrGlyGluGlnIleAspProSerThrHis-----ArgLysAsn 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGluValProTyrAlaArgSerGluAlaHisLeuThrGluLeuLeuGluGluValCys
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                                                                                                                                                                         ---GlyThrLeuLysPheAlaCysGluSerIleValGluGyrGluAspGluLeuIle 129
                                                                                                                                                                                                                                                                                                                                                                                             GAGCGGATCCTGGACTAT--------AGTGTTCACGCTGAGCGCAAGGGC
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Sequence 14, Application US/09724864 Patent No. 6380362

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Result
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-DB-Issued_patents_Na -QFMT-fastap -SUFFIX-rni -MINNATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-buman40.cdi
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-MANN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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seq length:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
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                                                                                                                                                                                                                        is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,
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847
1 RRSQDLHCGACRAL
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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 US-09-163-285-3

US-09-163-285-1

US-09-724-864-14

US-08-257-073-10

US-08-588-985-1

US-08-971-98-159

US-08-961-083-159

US-08-961-527-208

US-08-297-494-38

US-08-297-494-38

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                                                                                                                                                                                                                                                                                                                                  APPLICANT: Khodadou
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                 STATE: M
                                                                                                                                FILING DATE:
CLASSIFICATION:
                       TELEPHONE:
                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777
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                                                                                                                                                                                                                                        02109
                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                   28 State Street
                                                                                                                                                                                                                                                 USA
             (617)
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US-08-938-105-2 US-09-071-035-3 US-09-071-035-3 US-08-803-973-1 US-08-803-972-1 US-08-872-644-42 US-08-977-2749-42 US-08-297-494-42 US-08-297-510-42 US-08-479-532-42 US-08-479-532-42 US-08-455-525-42 US-08-455-525-42 US-08-455-525-42 US-08-455-525-42 US-08-894-017-24
5352450-1
US-08-961-527-148
US-09-470-512A-3
US-09-961-083-33
US-08-961-527-108
US-08-961-527-108 US-09-139-491-42 PCT-US92-03222-42 US-09-134-001C-578 US-08-837-029-1 US-08-750-152A-1 US-08-306-691B-21 PCT-US93-06251-25 Patent No Sequence Sequence
Sequence
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ALIGNMENTS

Sequence 3, Application US/09163285
Sequence 3, Application US/09163285
Patent No. 6204013
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 4
CORRESSORDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER: IBM PC COMPATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
OFFWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/163,285
FILING DATE:
CLASSIFICATION NUMBER: US/09/163,285
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
PRICE RENCE/DOCKET NUMBER: MNI-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)747-400
TELEPHONE: (617)727-7400

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Search completed: March 31, 2003, 11:59:14 Job time: 51.9767 secs

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US-10-142-419-173
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Best Local Similarity:
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C244
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary E.
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US-10-082-502-21 (1-162) x US-10-123-262-173 (1-1210)
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APPLICANT: Beresini, Mauree
APPLICANT: Berorge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Eller
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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CURRENT FILING DATE: 2002-04-15
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C38
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US-10-143-114-173
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1CZ11
CURRENT APPLICATION NUMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
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Goddard, Audrey
Godowski, Paul J.
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Sherwood, Steven
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Wood, William
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; TYPE: DNA
; ORGANISM: HOMO S
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SEQ ID NO 173
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GENERAL INFORMATION
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
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Gurney, Austin L.
Sherwood, Steven
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Wood,William
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US-10-142-431-173
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; Publication No. US200:
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Best Local Similarity:
Query Match:
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; ORGANISM: Homo Sapien
US-10-140-474-173
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 2002-05-06
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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           Application US/10142431
o. US20030036179A1
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; ORGANISM: Homo
US-10-142-431-173
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LENGTH: 1210
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C251
CURRENT APPLICATION NUMBER: US/10/142,431
CURRENT FILING DATE: 2002-05-10
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                                                                    ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
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                                    AspLysLeuCysSerLysArgThrAspLeuCysAspH1sAlaLeuH1sArgSerH1sAsp
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                        GACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATGAT
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary E.
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Filvaroff, Ellen
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DeForge, Laura
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GENERAL INFORMATION:

APPLICANT: Baker, Keyin P.

APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desonyers, Luc
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Georitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Sherwood, Steven,
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy
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Best Local Similarity:
Query Match:
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; ORGANISM: HOMO
US-10-176-921-173
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Publication No. US20030032155A1
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                          Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                            DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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RESULT 10
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; TYPE: DNA
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US-10-137-865-173
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                         Sequence 173, Applic Publication No. US20 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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             Gao, Wei-Qiang
Gerritsen, Mary
                                       Desnoyers, Luc
Filvaroff, Ellen
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DeForge, Laura
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NUMBER OF SEQ ID
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tunnas, Daniel
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DeForge, Laura
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Filvaroff, Ellen
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APPLICANT: Beresini, Mau
APPLICANT: Berosge, Laur
APPLICANT: Desnoyers, Lu
APPLICANT: Desnoyers, Lu
APPLICANT: Filvaroff, El
APPLICANT: Gao, Wei-Qian
APPLICANT: Gerritsen, Madr
APPLICANT: Gerritsen, Madr
APPLICANT: Godowski, Pau
APPLICANT: Godowski, Pau
APPLICANT: Sherwood, Ste
APPLICANT: Sherwood, Ste
APPLICANT: Smith, Victor
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                       APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watenabe, Colin K
APPLICANT: Watenabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C288
CURRENT EPELICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
Prior Application removed - NUMBER OF SEQ ID NOS: 550
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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RESULT 5
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APPLICANT: Beresini, Mauree
APPLICANT: Desorge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellean
APPLICANT: Gao, Wei-Glang
APPLICANT: Gerritsen, Mary
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C160
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Wood, William
Zhang, Zemin
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Filvaroff, Ellen
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NUMBER OF SEQ.I.
SEQ.ID NO 173
LENGTH: 1210
TYPE: DNA
ORGANISM: Homo
US-10-175-746-173
                      Percent Similarity:
Best Local Similarity:
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CURRENT FILING DATE: 2002-06-19
                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C353
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Wood, William
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Pred. No.:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 173
LENGTH: 1210
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Gurney, Austin L.
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; Prior Application removed - Si
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 173
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-904-173
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Best Local Similarity:
Query Match:
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US-10-123-904-173
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APPLICANT: Beresini, Mau
APPLICANT: DeForge, Laur
APPLICANT: Desnoyers, Lu
APPLICANT: Filvaroff, El
APPLICANT: Gao, Wei-Gian
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Wood, William
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Stewart, Timothy A.
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Filvaroff, Ellen
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R FILING DATE: 1998-06-11
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APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei Qiang
Gerritgen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                 Baker, Kevin P.
                                                       Tumas, Daniel
Watanabe, Colin K
                                               Watanabe, Col
Wood, William
                                                                            Smith, Victoria Stewart, Timothy
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PRIOR APPLICATION NUMBER: 60/0649911
PRIOR APILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
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-Q-Cgn2_1/USPTO_spool/USI0082502/runat_24032003_135103_6870/app_query.fasta_1.1308
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-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOF-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Sequence 309, App
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Sequence 173, App
                                                                                      Description
      ; ORGANISM: Homo sapiens US-09-864-864-309
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US-09-864-864-309
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jenr
APPLICANT: Harlocker, St
                                    NUMBER OF SEQ ID NOS: 341
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 309
LENGTH: 814
TYPE: DNA
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APPLICANT:
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APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steve P.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Benson, Darrin R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 110121.523
                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
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Harlocker, Susan L.
Dillon, Davin C.
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US-10-142-13-114-173
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US-10-142-13-262-173
US-10-142-423-173
US-10-142-423-173
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US-10-142-846-398
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US-10-174-573-479
US-10-174-582-479
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Sequence 174, App
Sequence 479, App
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Db	Qy	DЬ	VΩ	Дb	Оу	d d	Ωу	дb	δ	문	Qy	D b	Ω	망	Qy	문	Qy	US-10-	Query DB:
542	161	482	141	422	121	362	101	302	81	242	61	182	41	122	21	62	_	082	Match:
GAGCTA 547	GluLeu 162	GACAAACTTTG	AspLysLeuCy	GTGGAGGAATA	ValGluGluTy	CAAGGCATCCG	GlnGlyIleAr	CATCGCAAGAA	HisargLysası	CTGCTGGAGGA	LeuLeuGluGlu	GATGGCAGCCAG	AspGlySerGl	GAAATTGCCCAC	GluIleAlaAr	CGGAGGAGCCAC	ArgArgSerGl	-502-21 (1-1	ch:
		CAGTAAGCGAACAGA	9SerLysArgThrAs	CGAGGATGAACTCAT	rGluAspGluLeuIl	ATCGACTCAGATAT	yIleAspSerAspIl	CTACGTACGTGTAGT	TyrvalArgvalva	GATATGTGACCGGAT	.ValCysAspArgMe	TCAGTGGTGGAGGT	nSerValValGluVa	GTGGACCCCAAGAA	yValAspProLysLy	GATCTCCACTGTGG	nAspLeuHisCysGl	US-10-082-502-21 (1-162) x BM832828	97.99% 14
		TCTTTGTGACCATG	pLeuCysAspHisAl	TGAATTCTTTTCCC	eGluPhePheSerAı	TAGCGGCACCCTCA	eSerGlyThrLeuLy	GGGCCGGAATGGAGA	lSerArgAsnGlyGl	GAAGGAGTATGGGG	tLysGluTyrGlyGl	GCCTTATGCCCGCTC	lProTyrAlaArgSe	GACCATTCAGATGG	sThrIleGlnMetGl	AGCATGCAGGGCTCT	yAlaCysArgAlaLe	(1-588)	Indels: Gaps:
		GACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATGAT	AspLysLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisArgSerHisAsp	GTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGGCTGACAATGTTAAA	ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys	CAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATT	/sPheAlaCysGluSerIle	CATCGCAAGAACTACGTACGTGGGGCCGGAATGGAGAATCCAGTGAACTGGACCTA	LuSerSerGluLeuAspLeu	CTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGGAACAGATTGATCCTTCCACC	LeuLeuGluGluValCysAspArgMetLysGluTyrGlyGluGlnIleAspProSerThr	GATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCACCTCACAGAG	erGluAlaHisLeuThrGlu	GAAATTGCCCAGGTGGACCCCAAGAAGACCATTCAGATGGGATCTTTCCGGATCAATCCA	ySerPheArgIleAsnPro	CGGAGGAGCCAGGATCTCCACTGTGGAGCATGCAGGCTCTGGTGGATGAACTAGAATGG	ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp		00
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Search completed: March 31, 2003, 04:51:14 Job time : 1041.65 secs

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                                                             ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
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Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index Unpublished (1997)
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/db_xref="taxon:10090"
/clone="IMAGE:1548981"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
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/lab_host="DH10B"
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BM832828
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Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: yongsung@mail.kribb.re.kr
Plate: 11 row: B column: 03
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/cell_line="SNU-484"
/lab_host="Top10F'"
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/clone_lib="S5SNU484s1"
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/db_xref="taxon:9606"
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                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatin Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution informatic found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11294 row: c column: 07
High quality sequence start: 4
High quality sequence stop: 701.
Location/Qualifiers
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 709)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BI411532
BI411532.1 GI:15172455
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602965126F1 NCI_CGAP_Lu33
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Tissue Procurement: Gilbert Smith, Ph.D.
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:5120574"
/clone_lib="NCI_CGAP_Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pT7T3D-Pac (P
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    (Pharmacia)
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IMAGE:5120574\5',
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REFERENCE AUTHORS TITLE

NCI-CGAP http://www.ncbi:nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy

Project

(CGAP),

Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 549)

Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae;

Euteleostomi;
; Murinae; Mus

Mus musculus house mouse

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 14 BE198865 LOCUS

14

DEFINITION

ug83d11.yl Soares_mammary_gland_NMLMG Mus musculus IMAGE:158981 5' similar to WP:FO1F1.11 CE01224 ;, BE198865 BE198865.1 GI:8711034

CDNA mRNA

26-JUN-2000 clone sequence.

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                                                                                              HisargLysasnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu
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                                                                                        CACCGCAAGAACTACGTACGCGTCGTGAGCCGGAATGGAGAATCCAGTGAACTAGACTTA
GAGCTA
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                                                                                                                    HisArgLysAsnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu 100
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humph
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian
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Contact: Robert Strausberg, Ph.D.
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Plate: LLAM8523 row: e column: 01
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Mammalia; Eutheria;
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Clone distribution: MGC clone distribution information can
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
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1 ArgArgSerGlnAspLeuHisCysGlyAlaCysArgAlaLeuValAspGluLeuGluTrp
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Location/Qualifiers
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Tissue Procurement: Gilbert Smith,
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Contact: Hennig S

Contact: Hennig S

Laboraty 123, dept.Lehrach

Max-Planck-Institut fuer Molekulare Genetik

Ihnestr.63-73, D-14195 Berlin, Germany

Tel: +49 30 8413 1612

Tel: +49 30 8413 1612

Eax: +49 30 8413 1380

Email: hennig@molgen.mpg.de

EST's are made from clones being representatives of clone clusters.

Clone clusters were calculated from oligonucleotide fingerprints.
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muril 1 (bases 1 to 802)
Yahyawi,M., Hennig,S., Neidhardt,L., Radelof,U., Hermann,I Lehrach,H. and O'Brien,J.
Detection of a high number of novel genes in a 9-day mouse CDNA library normalised by oligonucleotide fingerprinting
                                                                                                                                                                                                             Mus
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                                                                                                 Unpublished (2001)
Contact: Hennig S
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RESULT 11
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mRNA sequence.
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BE309953.1 GI:
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BACKWARD: 5'-TAATACGACTCACTATAGGG-3'
Seq primer: 5'-ATTTAGGTGACTATAG-3'
High quality sequence stop: 802.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="ICRFp522B2440"
/clone_lib="Mouse 9-day fetus cDNA library ICRFp5
/tissue_type="whole embryo"
/dev_stage="embryonic 9-day"
/lab_host="E.coli, XLI blue"
/note="Vector: PSVSport1; Site_1: NotI; Site_2: Sitherary preparation by oligo_dT priming of RNA. C be ordered from the Resource Center in Berlin, http://www.rzpd.de."
13 a 206 c 243 g 159 t 1 others
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IMAGE:3486696 5',
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Seq primer: Ml3 Forward
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TAG_TISSUE=duodenum
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/note="Vector: p773D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; UI-R-EB1 is a non-normalized Rat Duodenum library (RDU) constructed in p73T7 PAC vector according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). The oligonucleotide used to prime first strand synthesis contained the sequence tag TGTGGTTCAT between the Not I cloning site and dT18 stretch. The Rat Deuodenum tissue was provided by Tom Freeman of the Sanger
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/db_xref="taxon:10116"
/clone="UI-R-EB1-Cle-b-02-0-UI"
/clone_1lb="UI-R-EB1"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized cartilage library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluLeu 162
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EQ210416 EQ210416 GI:20426881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 724)
Bonaldo, M.F., Lenno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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                                                                   156
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                                                                                                                                                                /note-*Organ: Femur and Tibla; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; UI-R-DYI is a normalized cDNA library containing the following tissue(s): Rat Cartilage from Femur and Tibla. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTAATGGACG. The Rat cartilage tissue was provided by Dr Jeff Stevens at the
                                                               TAG_TISSUE-cartilage
TAG_SEQ-CTAATGGACG"
1 206 c 157 g
                                                                                                                              TAG_LIB-UI-R-DY1
                                                                                                                                                    University of Iowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UI-R-DX1-co1-e-06-0-UI"
/clone_lib="UI-R-DX1"
/tlssue_type="cartilage"
/dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sprague-Dawley
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys
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                                                                                                                                                                                                                                                                                                                                                                         Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW919569 665 bp mRNA linear EST 25-EST350873 Rat gene index, normalized rat, norvegicus, Bento Rattus norvegicus cDNA clone RGIFZ11 5' end, mRNA sequence. AW919569 AW919569.1 GI:8085366 EST.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
Contact: Lee, NH
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M.,
Kerlavage, A.R. and Adams, M.D.
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2, Medical Center Drive,
: (301)-838-3529
: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                          primer: M13 Reverse
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                                                                                                                    /lab_host="SOLR"
/note="Vector: pBlueSrring
Khol: Reft="Tokkoll | Particular | Part
                                                                                                                                                                                                                     Bento Soares"
                                                                                                                                                                                                                                    /clone_lib="Rat gene index, normalized rat,
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/db_xref="taxon:10116"
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Sciurognathi; Muridae;
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le, spleen"
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Email: mosares@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
                                                                                                                                                                                                                                                                                                                                            UI-R-EB1-cle-b-02-0-UI.s1 UI-R-EB1 Rattus
UI-R-EB1-cle-b-02-0-UI 3', mRNA sequence.
                                                                           Contact: Soares, MB
Program for Rat Gene Discovery and
University of Iowa
451 Eckstein Medical Research Build
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                   1 (bases 1 to 674)
Bonaldo, M.F., Lenno
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                  Adachi, ... Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Haraka, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imoteni, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojina, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Misasaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Selto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shibata, Shibata, Y., S
                                                                                                                                           Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
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                                                                                                              Hayashizaki, Y.
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High-efficiency full-length cDNA cloning
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         (18-AUG-2000) Yoshihide Hayashizaki, The Institute
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              GluIleAlaArgValAspProLysLysThrIleGlnMetGlySerPheArgIleAsnPro 40
Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@ggc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details
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Fax:81-45-503-9216)
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VDPKKTIQMGSFRINPDGSQSVVEVPYARSEAHLTELLEEVCDRWKEYGEQIDPSTHR
KNYVRVVSRNGESSELDLQGIRIDSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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/db_xref="GI:12860333"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/strain="C57BL/6J"
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/clone="5330432A10"
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Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc:riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/) for
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of sequence
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                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:2810406L24"
                                                                                                                                         /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                             /dev_stage="10,
                                 /clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10, 11 days embryo"
                                                                                                           /clone="2810406L24"
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Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330432A10:transmembrane protein 4, full
                      AK019927.1 GI:12860332
HTC; CAP trapper.
                                                                             insert sequence.
AK019927
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/translation="MKCWGWLALLLGYLLGTAWARRSQDLHCGACRALYDELEWEIAR
/translation="MKCWGWLALLLGYLLGTAWARRSQDLHCGACRALYDELEWEDEXTHR
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evidence:ISS
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/protein_id="BAB28597.1"
/db_xref="GI:12850115"
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musculus (strain:C57BL/6J) adult male

pituitary gland cDNA to

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1 (bases 1 to 843)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
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ValGluGluTyrGluAspGluLeuIleGluPhePheSerArgGluAlaAspAsnValLys 140
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                                                                        Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus 10, 11 days embryo whole body cDNA,
enriched library, clone:2810406L24:transmembrane
                                                      Genome Res.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Rodentia;
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Kawai,J.,

Shinagawa, A.,

Shibata, K.,

Yoshino, M.,

Itoh, M.,

Ishii,Y.,

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BASE COUNT
ORIGIN
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AUTHORS
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VERSION
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                                                                                                                 Mouse mouse.

Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentla;
1 (bases 1 to 808)
                                                                                                                                                                                                                                                          BI408525
602964995F1 NCI_CGAP_Lu33
mRNA sequence.
BI408525
Unpublished (1999)
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert
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EST.
                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian
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Smith,
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                                                                          GlnGlyIleArgIleAspSerAspIleSerGlyThrLeuLysPheAlaCysGluSerIle
                                                                                                            HisArgLysAsnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu
                                                                                                                                   CAGGGCATCCGAATTGACTCAGATATCAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATT
                                                                                                  CACCGCAAGAACTACGTACGCGTCGTGAGCCGGAATGGAGAATCCAGTGAACTAGACTTA
                                 GTGGAAGAATACGAGGATGAGCTTATCGAATTCTTCTCCAGAGAGGCTGACAACGTTAAA
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cDNA Library Arrayed by: The I.M.A.G.E.
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DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution
Clone distribution: NCI-CGAP clone distribution
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                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus (strain:C57BL/6J) 10

mRNA, Clone_lib:RIKEN full-length
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria;
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    /protein_id="BAB25346.1"
/db_xref="GI:12841774"
                                                              transmembrane protein
                                                                                    putative
                                                                                                                                                                                                                                            /tissue_type="pancreas"
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/db_xref="MGD:MGI:1897650"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                          /gene="Tmem4"
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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                                                                                                                                                                                                 Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                      Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
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                                                     Japan
          (E-mail:genome-res@gsc.riken.go.jp,
ken.go.jp/, Tel:81-45-503-9222,
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HisargLysasnTyrValArgValValSerArgAsnGlyGluSerSerGluLeuAspLeu
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Please visit our web site (http://genome.gsc.riken.go.jp/)
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/translation="MKGWGWLALLLGVLLGTAWARRSQDLHCGACRALVDELEWEIAR
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KNYVRVVSRNGESSELDLGGINGSDISGTLKFACESIVEEYEDELIEFFSREADNVK
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/clone_lib="RIKEN full-len
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/db_xref="FANTOM_DB:2900022B12"
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-Q-/cgn2_1/USPTQ_spco1/US10082502/runat_24032003_135100_6599/app_query.fasta_1.1308
-DB-EST -QFMT-fastap -SUFFIX-rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blts -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL \
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN=0 -MAXLEN=2000000000
-USER-US10082502_eCGN_1_1_5425_erunat_24032003_135100_6599 -NCPU=6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

SOURCE	KEYWORDS	VERSION	ACCESSION			DEFINITION	LOCUS	AK013568	RESULT 1
Mus musculus (strain:C57BL/6J) adult male hippocampus cDNA to mRNA,	HTC; CAP trapper.	AK013568.1 GI:12850979	AK013568	insert sequence.	enriched library, clone:2900022B12:transmembrane protein 4, full	us cDNA, 1	AK013568 754 bp mRNA linear HTC 19-JAN-2002		

DURCE Mus musculus (strain:C57BL/6J) adult male hippocampus cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:290002B12.

ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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                  ASPLYSLeuCysSerLysArgThrAspLeuCysAspHisAlaLeuHisIleSer-HisAs 160
AGAGCTC 589
                                                                       342
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Search completed: March 30, 2003, 22:42:58 Job time: 130.151 secs

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